

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 17, 2006, 03:42:53 ; Search time 168.444 Seconds
(without alignments)
93.904 Million cell updates/sec

Title: US-09-830-972A-2_COPY_1090_1125
Perfect score: 175
Sequence: 1 LKPAVLMMVFTYVGFNLGLTLLILALISLFSIPVI 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: Geneseq21980s:*
2: Geneseq21990s:*
3: Geneseq22000s:*
4: Geneseq22010s:*
5: Geneseq22020s:*
6: Geneseq22030s:*
7: Geneseq22040s:*
8: Geneseq22050s:*
9: Geneseq22060s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	175	100.0	199	3 AAY71559	Aay71559 Rat Nogo
2	175	100.0	199	5 ABB81077	Abb81077 Rat Nogo
3	175	100.0	359	3 AAY71558	Aay71558 Rat Nogo
4	175	100.0	360	3 AAY71383	Aay71383 Rat neuro
5	175	100.0	360	5 ABB81076	Abb81076 Rat neuro
6	175	100.0	361	3 AAY71385	Aay71385 Alternati
7	175	100.0	379	7 ADB85283	Adb85283 Rat focce
8	175	100.0	403	3 AAY71563	Aay71563 Rat Nogo
9	175	100.0	522	3 AAY71312	Aay71312 Rat neuro
10	175	100.0	1162	3 AAY71557	Aay71557 Mus muscu
11	175	100.0	1162	8 ADT89537	Adt89537 Mouse Nog
12	175	100.0	1162	8 ADS99349	Ads99349 Mouse Nog
13	175	100.0	1163	3 AAY71310	Aay71310 Rat neuro
14	175	100.0	1163	3 AAY71384	Aay71384 Alternati
15	175	100.0	1163	5 ABB81074	Abb81074 Rat neuro
16	175	100.0	1163	8 ADO08105	Ado08105 Mouse pol
17	175	100.0	1163	8 ADO26399	Ado26399 Rat trunc
18	175	100.0	1163	8 ADP45572	Adp45572 Rat NogoA
19	175	100.0	1163	9 ADZ07609	Adz07609 Rat NogoA
20	174	99.4	175	2 AAW78194	Aaw78194 Human sec
21	174	99.4	199	2 AAW53947	Aaw53947 Human NSP
22	174	99.4	199	2 AAW78313	Aaw78313 Fragment
23	174	99.4	199	2 AAY35903	Aay35903 Extended
24	174	99.4	199	3 AAB12805	Aab12805 Human NSP

25	174	99.4	199	4	AAB82348	Human NOG
26	174	99.4	199	5	ABB81080	Human neu
27	174	99.4	199	7	ADK67504	Human RTN
28	174	99.4	199	8	ADP19211	Human sec
29	174	99.4	199	8	ADP67236	Human NOG
30	174	99.4	200	4	AAB64514	Human sec
31	174	99.4	291	4	AAM33484	Human pol
32	174	99.4	291	8	ADL31138	Human pro
33	174	99.4	373	3	AY53624	A bone ma
34	174	99.4	373	3	AY53695	Human MAG
35	174	99.4	373	3	AAB24242	Human NOG
36	174	99.4	373	3	AAB82350	Human NOG
37	174	99.4	373	5	AAM47954	Human RTN
38	174	99.4	373	5	ABG30937	Human pan
39	174	99.4	373	5	ABP68601	Human NOG
40	174	99.4	373	5	ABB81079	Human neu
41	174	99.4	373	7	ADI63044	Human apo
42	174	99.4	373	7	ADK67503	Human RTN
43	174	99.4	373	8	ADP67235	Human NOG
44	174	99.4	642	2	AAW58383	Human sec
45	174	99.4	642	4	AAB90682	Human BGI

ALIGNMENTS

RESULT 1

RAY71559
ID AAY71559 standard; protein; 199 AA.

XX AAY71559;

DT 02-NOV-2000 (first entry)

DE Rat Nogo C/Nogo A proteins derived fragment to construct mutant Nogo-C.
XX Rat; neurite growth inhibitor; Nogo A; Nogo C; neural cell; myelin; CNS;
XX central nervous system; neoplastic disease; antiproliferative; glioma;
XX antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
XX degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
XX hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
XX psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
XX structural plasticity; screening; mutant; mutain.

OS Rattus sp.

XX Key Location/Qualifiers
XX Region 1. .11
FT /note= "Corresponds to residues 40-50 of rat Nogo C
FT protein shown in AAY71312"

FT Region 12. .199
FT /note= "Corresponds to residues 975-1162 of rat Nogo A
FT protein shown in AAY71310"

WO200031235-A2.

PD 02-JUN-2000.

DP 05-NOV-1999; 99WO-US036160.

XX 06-NOV-1998; 98US-0107446P.

XX (SCHW/) SCHWAB M E.
XX (CHEN/) CHEN M S.

PI Schwab ME, Chen MS;

DR WPI; 2000-400052/34.

XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX of the central nervous system and inducing regeneration of neurons.

XX Example; Page; 122pp; English.

XX The patent relates to neurite growth inhibitor Nogo which is free of all
CC central nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic diseases of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, cranio-pharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The
CC animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which can
CC treat or prevent disorders or diseases of the CNS. The present sequence
CC is derived by fusing two fragments from rat Nogo C and Nogo A proteins.
CC The fragment is used in the construction of mutant Nogo-C which is
CC composed of His-tag/T7-tag/Nogo-C N-terminus (11 aa) + Nogo-A sequence aa
CC 975-1162. Nogo A deletion mutants were used for mapping the inhibitory
CC sites of Nogo protein. Major inhibitory region was identified in the Nogo
CC A sequence from amino acids 172-974, particularly amino acids 542-722. In
CC addition, N-terminal region 1-171 was found to be inhibitory to NRH 3T3
CC fibroblast spreading. Note: The present sequence is not given in the
CC specification but is derived from rat Nogo C sequence shown in AAY71312
CC and Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC However, the specification does not include sequences for these SEQ ID
CC numbers
XX

XX Sequence 199 AA;
SQ
Query Match 100.0%; Score 175; DB 3; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.8e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKFAVLMWVFTYVGAFLNGLLILALISLFSIPVI 36
DB 127 LKFAVLMWVFTYVGAFLNGLLILALISLFSIPVI 162

RESULT 2
ABB81077
ID ABB81077 standard; protein; 199 AA.
XX
AC ABB81077;
XX
DT 05-NOV-2002 (first entry)
XX
DE Rat neurotransmitter receptor protein Nogo-C.
XX
KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW central nervous system; peripheral nervous system; tranquilizer; Nogo;
KW vulnary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW neurotransmitter receptor; rat; receptor.
XX
OS Rattus norvegicus.
XX
PN US2002072493-A1.
XX
XX 13-JUN-2002.
XX
XX 28-JUN-2001; 2001US-00893348.
XX
XX 19-MAY-1998; 98IL-00124500.
XX 21-JUL-1998; 98WO-US014715.
XX 22-DEC-1998; 98US-00218277.
XX 19-MAY-1999; 99US-00314161.
XX

PA (YEDA) YEDA RES & DEV CO LTD.
XX
XX Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;
PI Moalem G;
XX
XX WPI; 2002-607255/65.
DR N-PSDB; ABB86600.
XX
XX Promoting nerve regeneration and preventing neuronal degeneration in the
PT central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides.
XX
XX Example 5; Page 48-49; 93pp; English.

XX The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or glioma. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease is
CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (Ig)A, and Igg gamma-
CC pathies, complications of various drugs (e.g. metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents the rat
CC neurotransmitter receptor protein Nogo-C, an example of NS-specific
CC antigen
XX

XX Sequence 199 AA;
SQ
Query Match 100.0%; Score 175; DB 5; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.8e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKFAVLMWVFTYVGAFLNGLLILALISLFSIPVI 36
DB 126 LKFAVLMWVFTYVGAFLNGLLILALISLFSIPVI 161

RESULT 3
AAV71558
ID AAV71558 standard; protein; 359 AA.
XX
XX AAV71558;
XX
XX 02-NOV-2000 (first entry)
XX
XX Rat Nogo A protein fragment used in the construction of mutant Nogo-B.
XX
XX Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
XX central nervous system; neoplastic disease; antiproliferative; glioma;
XX antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
XX degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
XX hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
XX psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
XX structural plasticity; screening; mutant; mutagen.

XX OS Rattus sp.
XX Key Location/Qualifiers
XX FT 1. .171
XX FT /note= "Corresponds to residues 1-171 of rat Nogo A
XX FT protein shown in AAY71310"
XX FT 172. .359
XX FT /note= "Corresponds to residues 975-1162 of rat Nogo A
XX FT protein shown in AAY71310"
XX WO200031235-A2.
XX 02-JUN-2000.
XX 05-NOV-1999; 99WO-US026160.
XX 06-NOV-1998; 98US-0107446P.
XX (SCHW/) SCHWAB M E.
XX (CHEN/) CHEN M S.
XX Schwab ME, Chen MS;
XX WPI; 2000-400052/34.
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX of the central nervous system and inducing regeneration of neurons.
XX Example; Page; 122pp; English.
XX The patent relates to neurite growth inhibitor Nogo which is free of all
XX central nervous system (CNS) myelin material with which it is natively
XX associated. Nogo proteins and fragments displaying neurite growth
XX inhibitory activity are used in the treatment of neoplastic disease of
XX the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
XX ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
XX oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and
XX degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
XX Therapeutics which promote Nogo activity can be used to treat or prevent
XX hyperproliferative or benign dysproliferative disorders e.g. psoriasis
XX and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
XX used to inhibit production of Nogo protein to induce regeneration of
XX neurons or to promote structural plasticity of the CNS in disorders where
XX neurite growth, regeneration or maintenance are deficient or desired. The
XX animal models can be used in diagnostic and screening methods for
XX treat or prevent disorders and to screen for or test molecules which can
XX predisposition to disorders and diseases of the CNS. The present sequence
XX is derived by fusing two fragments of rat Nogo A protein shown in
XX AAY71310. The fragment is used in the construction of mutant Nogo-B. The
XX mutant is composed of His-tag/T7-tag/vector/Nogo-A sequence aa 1-171 +
XX 975-1162. Nogo A deletion mutants were used for mapping the inhibitory
XX sites of Nogo protein. Major inhibitory region was identified in the Nogo
XX A sequence from amino acids 172-974, particularly amino acids 542-722. In
XX addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3
XX fibroblast spreading. Note: The present sequence is not given in the
XX specification but is derived from rat Nogo A sequence shown in AAY71310.
XX SEQ ID number 35-42 are referred in claim 32 and SEQ ID NO: 29 in
XX disclosure of the specification. However, the specification does not
XX include sequences for these SEQ ID numbers
XX Sequence 359 AA;

Query Match 100.0%; Score 175; DB 3; Length 359;
Best Local Similarity 100.0%; Freq. No. 7.2e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKFAVLMVFTYVGLPFGNLTLLILALISLFSIPVI 36
Db 287 LKFAVLMVFTYVGLPFGNLTLLILALISLFSIPVI 322

RESULT 4

XX AAY71383
XX ID AAY71383 standard; protein; 360 AA.
XX AC AAY71383;
XX DT 02-NOV-2000 (first entry)
XX DE Rat neurite growth inhibitor Nogo B.
XX KW Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS;
XX central nervous system; neoplastic disease; antiproliferative; glioma;
XX antisense gene therapy; neuroblastoma; meningioma; retinoblastoma; base;
XX degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
XX hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
XX psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
XX structural plasticity; screening.
XX Rattus sp.
XX OS
XX Key Location/Qualifiers
XX FT 1. .172
XX FT /note= "Corresponds to amino acids 1-172 of Nogo A
XX FT protein shown in AAY71310"
XX FT Inhibitory-site 1. .171
XX FT /note= "Inhibits NIH 3T3 fibroblast spreading"
XX FT Modified-site 30
XX FT /note= "Casein kinase II site"
XX FT Region 31. .58
XX FT /note= "Acidic region"
XX FT Region 173. .360
XX FT /note= "Corresponds to C-terminal 188 amino acids
XX FT (residues 976-1163) of Nogo A protein (AAY71310). This
XX FT region is common to Nogo A, B and C isoforms"
XX FT Domain 185. .220
XX FT /label= "Transmembrane domain
XX FT /note= "C-terminal hydrophobic region"
XX FT Modified-site 221
XX FT /note= "Protein kinase C (PKC) site"
XX FT Modified-site 268. .270
XX FT /note= "Asn is N-glycosylated"
XX FT Modified-site 270
XX FT /note= "Protein kinase C (PKC) site"
XX FT Modified-site 286
XX FT /note= "Protein kinase C (PKC) site"
XX FT Domain 287. .322
XX FT /label= "Transmembrane domain
XX FT /note= "C-terminal hydrophobic region"
XX FT Modified-site 338. .340
XX FT /note= "Asn is N-glycosylated"
XX FT Modified-site 340
XX FT /note= "Protein kinase C (PKC) site"
XX WO200031235-A2.
XX 02-JUN-2000.
XX 05-NOV-1999; 99WO-US026160.
XX 06-NOV-1998; 98US-0107446P.
XX (SCHW/) SCHWAB M E.
XX (CHEN/) CHEN M S.
XX Schwab ME, Chen MS;
XX WPI; 2000-400052/34.
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX of the central nervous system and inducing regeneration of neurons.
XX Example; Page; 122pp; English.
XX The present sequence is a rat Nogo B protein which is a potent neural

cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. The Nogo B transcript arises as a result of alternative splicing of Nogo gene. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribosomes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: The present sequence is not given in the specification but is derived from Nogo A protein sequence (AA717110) and corresponds to residues 1-172 fused to 976-1163 of Nogo A. The specification claims an alternative version of this sequence (see AA71385.) which corresponds to residues 1-172 fused to 975-1163 of Nogo A. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However the specification does not include sequences for these SEQ ID numbers

Sequence 360 AA:

Seq	Sequence	360 AA;	Query Match	100.0%;	Score 175;	DB 3;	Length 360;
			Best Local Similarity	100.0%;	Pred. No. 7.2e-15;		
			Matches	36;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	LKFAVLMVFTTVVGGALFNGLTLLTLLILSLSP	36				
DB	287	LKFAVLMVFTTVVGGALFNGLTLLTLLILSLSP	322				

RESULT 5
ABB81076
ID ABB81076 standard; protein; 360 AA.

05-NOV-2002 (first entry)

Rat neurotransmitter receptor protein Noqo-B.

XX Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW central nervous system; peripheral nervous system; tranquilizer; Nogo;
KW ventral; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW neurotropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW osteopathologic; vasotropic; nephrotoxic; cytostatic; antigen; gene therapy;
KW neurotransmitter receptor; rat; receptor.

XX
OS *Rattus norvegicus*.

XX
PN
US2002072493-A1.

XX
PD 13-JUN-2002.

XX
PF
28-JUN-2001: 2001US-00893348.

XX
PR 19-MAY-1998: 98IL-00124500.

PR 21-JUL-1998; 98WO-US014715.
PR 22-DEC-1998: 98US-00218277.

PR 19-MAY-1999; 99US-00314161.
XX

PA (YEDA) YEDA RES & DEV CO LTD
XX

PI Eisenbach-Schwartz M, Hauben :
PI Moalem G:

XX
DR
WPI: 2002-607255/65.

7

DR	N-PSDB; AEN86600.
XX	
PT	Promoting nerve regeneration and preventing neuronal degeneration in the
PT	central/peripheral nervous system from injury/disease, comprises
PT	administering nervous system-specific activated T cells/antigen, or
PT	analogues/peptides.

Example 5; Page 47-48; 93pp; English.

The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering NS-specific activated T cells, NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or damages caused by surgery such as tumour excision. The disease is not an autoimmune disease or neoplasm. The disease results in a degenerative process occurring in either gray or white matter or both. The disease is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's disease, facial nerve (Bell's) palsy, Glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-artritic optic neuropathy, and vitamin deficiency, intervertebral disc herniation, prion diseases such as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral neuropathies associated with various diseases, including but not limited to uremia, porphyria, hypoglycemia, Sjogren larsen syndrome, acute sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary amyloidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-pathies, complications of various drugs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia telangiectasia, Friedreich's ataxia, amyloid polynuropathies, adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's disease, or lipoproteinemia. The present sequence represents the rat neurotransmitter receptor protein Nogo-B, an example of NS-specific antigen.

XX
SQ
Sequence 360 AA;

Query Match 100.0%; Score 175; DB 5; Length 360;
Best Local Similarity 100.0%; Pred. No. 7.2e-16;
Matches 36; Conservative 0; Mismatches 0; Indels

Qy	1	LKFAVLMMWFTTVVGALENGLTLLILALISLFSIPVI	36
Db	287	LKFAVLMMWFTTVVGALENGLTLLILALISLFSIPVI	322

RESULT 6

AA71385
ID AA71385

XX
AC
AA71385;

XX	
DT	02-NOV-2000 (first entry)

Alternative version of rat neurite growth inhibitor Nogo B.

XX OS Rattus sp.

XX	Key	Location/Qualifiers
FH		

Region
ET
ET

FT Misc-difference 371 /note= "Encoded by TAG"
 FT Misc-difference 371 /note= "Encoded by TGA"
 FT Misc-difference 374 /note= "Encoded by TAG"
 FT Misc-difference 380 /note= "Encoded by TAA"
 FT Misc-difference 406 /note= "Encoded by TAA"
 FT Misc-difference 408 /note= "Encoded by TAG"
 FT Misc-difference 410 /note= "Encoded by TAA"
 FT Misc-difference 422 /note= "Encoded by TAA"
 FT Misc-difference 433 /note= "Encoded by TGA"
 FT Misc-difference 440 /note= "Encoded by TAG"
 FT Misc-difference 453 /note= "Encoded by TAG"
 FT Misc-difference 465 /note= "Encoded by TAG"
 FT Misc-difference 482 /note= "Encoded by TAG"
 FT Misc-difference 513 /note= "Encoded by TAA"
 FT XX WO2000031235-A2.
 XX PD 02-JUN-2000.
 XX PF 05-NOV-1999; 99WO-US026160.
 XX PR 06-NOV-1998; 98US-0107446P.
 XX PA (SCHW/) SCHWAB M E.
 XX PA (CHEN/) CHEN M S.
 XX PI Schwab ME, Chen MS;
 XX DR WPI; 2000-400052/34.
 XX DR N-PSDB; RAD01175.
 XX PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
 XX PT of the central nervous system and inducing regeneration of neurons.
 XX PS Claim 7; Fig 14; 122pp; English.
 XX CC The present sequence is a rat Nogo C protein which is a potent neural
 XX CC cell growth inhibitor and is free of all central nervous system (CNS)
 XX CC myelin material with which it is natively associated. Nogo proteins and
 XX CC fragments displaying neurite growth inhibitory activity are used in the
 XX CC treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,
 XX CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma, glioblastoma,
 XX CC haemangioblastoma, acoustic neuroma, oligodendroglioma, menangioma,
 XX CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
 XX CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
 XX CC activity can be used to treat or prevent hyperproliferative or benign
 XX CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
 XX CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit
 XX CC production of Nogo protein to induce regeneration of neurons or to
 XX CC promote structural plasticity of the CNS in disorders where neurite
 XX CC growth, regeneration or maintenance are deficient or desired. The animal
 XX CC models can be used in diagnostic and screening methods for predisposition
 XX CC to disorders and to screen for or test molecules which can treat or
 XX CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
 XX CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
 XX CC these SEQ ID numbers
 XX CC Sequence 522 AA;
 XX SQ

Query Match 100.0%; Score 175; DB 3; Length 522;
 Best Local Similarity 100.0%; Pred. No. 1.le-15;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKFAVIMMVFTYVGALFNGLTLLILALISLFSIPVI 36
 DB 165 LKFAVIMMVFTYVGALFNGLTLLILALISLFSIPVI 200
 RESULT 10
 AAY71557
 ID AAY71557 standard; protein; 1162 AA.
 XX AC AAY71557;
 XX DT 02-NOV-2000 (first entry)
 XX DE Rat Nogo A truncated protein used in the construction of mutant Nogo-A.
 KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening; mutant; mutein.
 XX OS Rattus sp.
 XX XX WO2000031235-A2.
 XX PD 02-JUN-2000.
 XX PF 05-NOV-1999; 99WO-US026160.
 XX PR 06-NOV-1998; 98US-0107446P.
 XX PA (SCHW/) SCHWAB M E.
 XX PA (CHEN/) CHEN M S.
 XX PI Schwab ME, Chen MS;
 XX DR WPI; 2000-400052/34.
 XX PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
 XX PT of the central nervous system and inducing regeneration of neurons.
 XX PS Example; Page; 122pp; English.
 XX CC The patent relates to neurite growth inhibitor Nogo which is free of all
 XX CC central nervous system (CNS) myelin material with which it is natively
 XX CC associated. Nogo proteins and fragments displaying neurite growth
 XX CC inhibitory activity are used in the treatment of neoplastic disease of
 XX CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
 XX CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
 XX CC oligodendroglioma, menangioma, neuroblastoma or retinoblastoma and
 XX CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
 XX CC Therapeutics which promote Nogo activity can be used to treat or prevent
 XX CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
 XX CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can
 XX CC be used to inhibit production of Nogo protein to induce regeneration of
 XX CC neurons or to promote structural plasticity of the CNS in disorders where
 XX CC neurite growth, regeneration or maintenance are deficient or desired. The
 XX CC animal models can be used in diagnostic and screening methods for
 XX CC predisposition to disorders and to screen for or test molecules which can
 XX CC treat or prevent disorders or diseases of the CNS. The present sequence
 XX CC is a truncated form of rat Nogo A protein shown in AAY71310, which is
 XX CC used in the construction of mutant Nogo-A. Nogo-A is composed of His-
 XX CC tag/77-tag/vector/Nogo-A sequence aa 1-1162. Nogo A deletion mutants were
 XX CC used for mapping the inhibitory sites of Nogo protein. Major inhibitory
 XX CC region was identified in the Nogo A sequence from amino acids 172-974.
 XX CC Particularly amino acids 542-722. In addition, N-terminal region 1-171
 XX CC was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The

CC present sequence is not given in the specification but is derived from
CC rat Nogo A sequence shown in AA71310. SEQ ID numbers 35-42 are referred
CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC However, the specification does not include sequences for these SEQ ID
CC numbers
XX
SQ Sequence 1162 AA;
Query Match 100.0%; Score 175; DB 3; Length 1162;
Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
DB 1090 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1125
RESULT 11
ADT89537
ID ADT89537 standard; protein; 1162 AA.
XX
AC ADT89537;
XX
DT 16-DEC-2004 (first entry)
XX
DE Mus musculus Nogo protein.
XX
KW Nerve regeneration; gene therapy; vaccine; neuroprotective; neurotropic;
KW Nogo; mouse.
XX
OS Mus musculus.
XX
PN US2004191240-A1.
XX
PD 30-SEP-2004.
XX
PF 31-JUL-2003; 2003US-00633423.
XX
PR 28-MAR-2003; 2003JP-00092923.
PR 30-APR-2003; 2003US-00427741.
XX
PA (TOHY/) TOHYAMA M.
PA (YAMA/) YAMASHITA T.
XX
PI Tohyama M, Yamashita T;
XX
WPI; 2004-698659/68.
DR N-PSDB; ADT89536.
XX
PT Regenerating nerves or modulating nerve regeneration comprises inhibiting
PT or modulating p75 signal transduction pathway by administering a
PT transduction agent, e.g. p21 or Rho, or an agent that interacts with the
PT transduction agent.
XX
PS Example 2; SEQ ID NO 10; 209pp; English.
XX
CC The present invention relates to a method for regenerating nerves or
CC modulating nerve regeneration. The method involves inhibiting or
CC modulating a p75 signal transduction pathway. The invention is useful for
CC treating, preventing or diagnosing neurological diseases based on nerve
CC regeneration and for identifying agents useful for nerve regeneration.
CC The invention is also useful in gene therapy and for preparing vaccine.
CC The present sequence is the Mus musculus Nogo protein. Note: this
CC sequence is said to be encoded by SEQ ID NO 9, however this does not appear
CC to be the same.
XX
SQ Sequence 1162 AA;
Query Match 100.0%; Score 175; DB 8; Length 1162;
Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36

DB 1089 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1124
RESULT 12
ADS99349
ID ADS99349 standard; protein; 1162 AA.
XX
AC ADS99349;
XX
DT 30-DEC-2004 (first entry)
XX
DE Mouse Nogo protein - SEQ ID 10.
XX
KW nerve regeneration; neurological disease; Pep5; Rho GDI; Rho; Rho kinase;
KW disease; nervous disorder; nervous condition; spinal cord injury;
KW cerebrovascular disorder; brain injury; neurite outgrowth inhibition;
KW neuron network construction; Nogo.
XX
OS Mus musculus.
XX
PN WO2004087744-A2.
XX
PD 14-OCT-2004.
XX
PF 26-MAR-2004; 2004WO-JP004385.
XX
PR 28-MAR-2003; 2003JP-00092923.
PR 30-APR-2003; 2003JP-00125681.
PR 31-JUL-2003; 2003JP-00284559.
XX
PA (INTE-) INTELLECTUAL PROPERTY CONSULTING INC.
XX
PI Tohyama M, Yamashita T, Tanaka H, Higuchi H;
XX
WPI; 2004-729217/71.
DR N-PSDB; ADS99348.
XX
PT New composition for regenerating nerves or treating neurological diseases
PT comprises a polypeptide (e.g. Pep5 or PKC) involved in p75 signal
PT transduction pathway, or an agent that interacts with the polypeptide to
PT block the pathway.
XX
PS Disclosure; SEQ ID NO 10; 613pp; English.
XX
CC The invention comprises a composition for regenerating nerves and
CC treating neurological diseases. The composition of the invention contains
CC a Pep5 polypeptide and an agent capable of interacting with a Rho GDI,
CC Rho, or Rho kinase polypeptide. The composition of the invention is
CC useful for treating, preventing, diagnosing, or prognosing nervous
CC disease/disorders/conditions, such as: spinal cord injury,
CC cerebrovascular disorders or brain injury. The composition of the
CC invention may also be used for disrupting or reducing inhibition of
CC neurite outgrowth or for constructing a network of neurons. In addition,
CC the composition may further be used to identify agents that may treat
CC neurological diseases or induce nerve regeneration. The present amino
CC acid sequence represents a mouse Nogo protein that was used in the
CC exemplification of the invention.
XX
SQ Sequence 1162 AA;
Query Match 100.0%; Score 175; DB 8; Length 1162;
Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
DB 1089 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1124
RESULT 13
AA71310
ID AA71310 standard; protein; 1163 AA.

XX AC AAY711310;
XX DT 02-NOV-2000 (first entry)
XX DE Rat neurite growth inhibitor Nogo A.
XX KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
XX KW central nervous system; neoplastic disease; antiproliferative; glioma;
XX KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
XX KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
XX KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
XX KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
XX KW structural plasticity; screening.
XX OS Rattus sp.
XX PH Key Location/Qualifiers
XX FT Inhibitory-site 1..171 /note= "Inhibits NIH 3T3 fibroblast spreading"
XX FT Modified-site 30 /note= "Casein kinase II site"
XX FT Region 31..58 /note= "Acidic region"
XX FT Region 31..57 /note= "Region specifically described in claim 16"
XX FT Region 172..259 /note= "This region is not essential for inhibitory activity"
XX FT Modified-site 233 /note= "Protein kinase C (PKC) site"
XX FT Modified-site 242..244 /note= "Asn is N-glycosylated"
XX FT Modified-site 291 /note= "Protein kinase C (PKC) site"
XX FT Modified-site 295 /note= "Protein kinase C (PKC) site"
XX FT Misc-difference 404 /note= "Encoded by TTG"
XX FT Modified-site 436 /note= "Protein kinase C (PKC) site"
XX FT Modified-site 468..470 /note= "Asn is N-glycosylated"
XX FT Modified-site 484 /note= "Protein kinase C (PKC) site"
XX FT Modified-site 488 /note= "Protein kinase C (PKC) site"
XX FT Modified-site 502 /note= "Casein kinase II site"
XX FT Inhibitory-site 542..722 /note= "Casein kinase II site"
XX FT Modified-site 723..640 /note= "used as immunogen to generate antibody AS 472"
XX FT Peptide 628 /note= "Protein kinase C (PKC) site"
XX FT Modified-site 694..696 /note= "Asn is N-glycosylated"
XX FT Modified-site 715 /note= "Casein kinase II site"
XX FT Peptide 762..1163 /note= "used as immunogen to generate antibody AS Bruna"
XX FT Modified-site 784 /note= "Protein kinase C (PKC) site"
XX FT Modified-site 821 /note= "Protein kinase C (PKC) site"
XX FT Modified-site 850 /note= "Protein kinase C (PKC) site"
XX FT Modified-site 855 /note= "Protein kinase C (PKC) site"
XX FT Modified-site 863 /note= "Casein kinase II site"
XX FT Modified-site 868

FT Modified-site /note= "Protein kinase C (PKC) site"
FT Modified-site /note= "Protein kinase C (PKC) site"
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site /note= "PKC and casein kinase II sites"
FT Modified-site /note= "PKC and casein kinase II sites"
FT Region /note= "This region is not essential for inhibitory activity"
FT Region /note= "C-terminal common region found in Nogo A, B and C isoforms"
FT Domain 988..1023 /label= "Transmembrane domain"
FT /note= "C-terminal hydrophobic region specifically described in claim 16"
FT Modified-site /note= "Protein kinase C (PKC) site"
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site /note= "Protein kinase C (PKC) site"
FT Modified-site /note= "Protein kinase C (PKC) site"
FT Domain 1089 /note= "Protein kinase C (PKC) site"
FT /note= "C-terminal hydrophobic region specifically described in claim 16"
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site /note= "Protein kinase C (PKC) site"
XX PN WO200031235-A2.
XX PD 02-JUN-2000.
XX PF 05-NOV-1999; 99WO-US026160.
XX PR 06-NOV-1998; 98US-0107446P.
XX PA (SCHW/) SCHWAB M E.
XX PA (CHEN/) CHEN M S.
XX XX Schwab ME, Chen MS;
XX PI WPI; 2000-400052/34.
XX DR N-PSDB; AAD01173.
XX XX Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.
XX PS Claim 3; Fig 2A; 122pp; English.
XX CC The present sequence is a rat Nogo A protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. The protein was derived from a cDNA generated by fusing R018U37-3, R1-3U21 cDNAs isolated from hexanucleotides primed rat brain stem/spinal cord library, and O1118 cDNA from an oligo (dT)-primed rat oligodendrocyte library. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, meningioma, haemangioblastoma, acoustic neuroma, oligodendroglioma, menangioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy.

FT Modified-site /note= "Asn is N-glycosylated"
 FT 1143
 FT /note= "Protein kinase C (PKC) site"
 XX
 PN WO200031235-A2.
 XX
 PD 02-JUN-2000.
 XX
 XX 05-NOV-1999; 99WO-US026160.
 XX
 XX 06-NOV-1998; 98US-0107446P.
 XX
 XX (SCHWAB) SCHWAB M E.
 XX (CHEN) CHEN M S.
 XX
 XX Schwab ME, Chen MS;
 XX
 XX WPI; 2000-400052/34.
 XX
 XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
 XX of the central nervous system and inducing regeneration of neurons.
 XX
 XX Claim 3; Fig 13; 122pp; English.
 XX
 XX The present sequence is an alternative version of rat Nogo A protein
 XX which is a potent neural cell growth inhibitor and is free of all central
 XX nervous system (CNS) myelin material with which it is native
 XX associated. Nogo proteins and fragments displaying neurite growth
 XX inhibitory activity are used in the treatment of neoplastic disease of
 XX the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
 XX ependyma, pinealoma, haemangioblastoma, acoustic neuroma,
 XX oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and
 XX degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
 XX Therapeutics which promote Nogo activity can be used to treat or prevent
 XX hyperproliferative or benign dysproliferative disorders e.g. psoriasis
 XX and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
 XX used to inhibit production of Nogo protein to induce regeneration of
 XX neurons or to promote structural plasticity of the CNS in disorders where
 XX neurite growth, regeneration or maintenance are deficient or desired. The
 XX animal models can be used in diagnostic and screening methods for
 XX predisposition to disorders and to screen for or test molecules which can
 XX treat or prevent disorders or diseases of the CNS. Note: The present
 XX sequence is an alternative version of the Nogo A sequence shown in Fig.
 XX 2A (see AAY71310). SEQ ID numbers 35-42 are referred in claim 32 and SEQ
 XX ID NO: 29 in disclosure of the specification. However the specification
 XX does not include sequences for these SEQ ID numbers
 XX
 XX Sequence 1163 AA;
 XX
 XX Query Match 100.0%; Score 175; DB 3; Length 1163;
 XX Best Local Similarity 100.0%; Pred. No. 2,7e-15;
 XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 LKFAVLMMWFTTVGALFNGLLTLLILALISLPSIPVI 36
 XX |||||
 XX Db 1090 LKFAVLMMWFTTVGALFNGLLTLLILALISLPSIPVI 1125
 XX
 XX RESULT 15
 XX ABB81074
 XX ID ABB81074 standard; protein; 1163 AA.
 XX
 XX AC ABB81074;
 XX
 XX DT 05-NOV-2002 (first entry)
 XX
 XX DE Rat neurotransmitter receptor protein Nogo-A.
 XX
 XX KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
 XX central nervous system; peripheral nervous system; tranquilizer; Nogo;
 XX vulnerable; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
 XX neurotropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;

KW neurotransmitter receptor; rat; receptor.
 XX
 XX Rattus norvegicus.
 XX
 XX US2002072493-A1.
 XX
 XX PD 13-JUN-2002.
 XX
 XX 28-JUN-2001; 2001US-00893348.
 XX
 XX 19-MAY-1998; 98IL-00124500.
 XX 21-JUL-1998; 98WO-US014715.
 XX 22-DEC-1998; 98US-00218277.
 XX 19-MAY-1999; 99US-00314161.
 XX
 XX (YEDA) YEDA RES & DEV CO LTD.
 XX
 XX Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;
 XX Moalem G;
 XX
 XX WPI; 2002-607255/65.
 XX
 XX N-PSDB; AEN86600.
 XX
 XX Promoting nerve regeneration and preventing neuronal degeneration in the
 XX central/peripheral nervous system from injury/disease, comprises
 XX administering nervous system-specific activated T cells/antigen, or
 XX analogs/peptides.
 XX
 XX Example 5; Page 44-47; 93pp; English.
 XX
 XX The invention relates to promoting nerve regeneration or conferring
 XX neuroprotection and preventing or inhibiting neuronal degeneration in the
 XX central/peripheral nervous system (NS). The method involves administering
 XX NS-specific activated T cells, NS-specific antigen, its analogue or its
 XX peptide, a nucleotide sequence the NS-specific antigen or its analogue or
 XX combinations. The method is useful for promoting nerve regeneration and
 XX preventing neuronal degeneration in central/peripheral nervous system
 XX from injury/disease, where the injury is spinal cord injury, blunt
 XX trauma, penetrating trauma, hemorrhagic stroke, ischemic stroke or
 XX damages caused by surgery such as tumour excision. The disease is not an
 XX autoimmune disease or neoplasm. The disease results in a degenerative
 XX process occurring in either gray or white matter or both. The disease is
 XX diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
 XX disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
 XX amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
 XX vitamin deficiency, intervertebral disc herniation, prion diseases such
 XX as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
 XX neuropathies associated with various diseases, including but not limited
 XX to uremia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute
 XX sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
 XX amyloidosis, obstructive lung diseases, acromegaly, malabsorption
 XX syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
 XX pathies, complications of various drugs (e.g., metronidazole) and toxins
 XX (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
 XX telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,
 XX adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
 XX disease, or lipoproteinemia. The present sequence represents the rat
 XX neurotransmitter receptor protein Nogo-A, an example of NS-specific
 XX antigen
 XX
 XX SQ Sequence 1163 AA;
 XX
 XX Query Match 100.0%; Score 175; DB 5; Length 1163;
 XX Best Local Similarity 100.0%; Pred. No. 2,7e-15;
 XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 LKFAVLMMWFTTVGALFNGLLTLLILALISLPSIPVI 36
 XX |||||
 XX Db 1090 LKFAVLMMWFTTVGALFNGLLTLLILALISLPSIPVI 1125
 XX
 XX Search completed: February 17, 2006, 03:49:30
 XX Job time : 169.444 secs

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Tue Feb 21 15:13:27 2006


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submitted to the EMBL Data Library, August 1996
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A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2484 <WIL>
A:Cross-references: UNIPROT:Q9U347; UNIPARC:UPI00000827B8; EMBL:Z78066; PIDN:CAB51467.1;
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3c
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2
Query Match 55.4%; Score 97; DB 2; Length 2484;
Best Local Similarity 41.7%; Pred. No. 0.0015;
Matches 15; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2403 IKFGLVMSLTYIASWFSGFTLAILGLGVFSVPKV 2438

RESULT 6
T26215
hypothetical protein W06A7.3a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2607 <WIL>
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A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3a
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2
Query Match 55.4%; Score 97; DB 2; Length 2607;
Best Local Similarity 41.7%; Pred. No. 0.0015;
Matches 15; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2526 IKFGLVMSLTYIASWFSGFTLAILGLGVFSVPKV 2561

RESULT 7
T05595
hypothetical protein F9D16.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
A:Accession: T05595
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-275 <BEV>
A:Cross-references: UNIPROT:Q5SUR3; UNIPARC:UPI00000822F; EMBL:AL035394
A:Experimental source: cultivar Columbia; BAC clone F9D16
C:Genetics:
A:Gene: CESP:T05595
A:Map position: 4
A:Introns: 89/1; 149/2; 196/3; 220/1
A>Note: F9D16.100
Query Match 43.7%; Score 76.5; DB 2; Length 275;
Best Local Similarity 40.5%; Pred. No. 0.059;
Matches 15; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

submitted to the EMBL Data Library, August 1996
A:Reference number: Z20173
A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2484 <WIL>
A:Cross-references: UNIPROT:Q9U347; UNIPARC:UPI00000827B8; EMBL:Z78066; PIDN:CAB51467.1;
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3c
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2
Query Match 55.4%; Score 97; DB 2; Length 2484;
Best Local Similarity 41.7%; Pred. No. 0.0015;
Matches 15; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2403 IKFGLVMSLTYIASWFSGFTLAILGLGVFSVPKV 2438

RESULT 6
T26215
hypothetical protein W06A7.3b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2607 <WIL>
A:Cross-references: UNIPROT:Q23187; UNIPARC:UPI000007623E; EMBL:Z78066; PIDN:CAB01522.2;
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3a
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2
Query Match 55.4%; Score 97; DB 2; Length 2607;
Best Local Similarity 41.7%; Pred. No. 0.0015;
Matches 15; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2526 IKFGLVMSLTYIASWFSGFTLAILGLGVFSVPKV 2561

RESULT 7
T05595
hypothetical protein F9D16.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
A:Accession: T05595
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-275 <BEV>
A:Cross-references: UNIPROT:Q5SUR3; UNIPARC:UPI00000822F; EMBL:AL035394
A:Experimental source: cultivar Columbia; BAC clone F9D16
C:Genetics:
A:Gene: CESP:T05595
A:Map position: 4
A:Introns: 89/1; 149/2; 196/3; 220/1
A>Note: F9D16.100
Query Match 43.7%; Score 76.5; DB 2; Length 275;
Best Local Similarity 40.5%; Pred. No. 0.059;
Matches 15; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

submitted to the EMBL Data Library, August 1996
A:Reference number: Z20173
A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2484 <WIL>
A:Cross-references: UNIPROT:Q9U347; UNIPARC:UPI00000827B8; EMBL:Z78066; PIDN:CAB51467.1;
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3c
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2
Query Match 55.4%; Score 97; DB 2; Length 2484;
Best Local Similarity 41.7%; Pred. No. 0.0015;
Matches 15; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2403 IKFGLVMSLTYIASWFSGFTLAILGLGVFSVPKV 2438

RESULT 6
T26215
hypothetical protein W06A7.3b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2607 <WIL>
A:Cross-references: UNIPROT:Q23187; UNIPARC:UPI000007623E; EMBL:Z78066; PIDN:CAB01522.2;
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3a
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2
Query Match 55.4%; Score 97; DB 2; Length 2607;
Best Local Similarity 41.7%; Pred. No. 0.0015;
Matches 15; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2526 IKFGLVMSLTYIASWFSGFTLAILGLGVFSVPKV 2561

RESULT 7
T05595
hypothetical protein F9D16.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
A:Accession: T05595
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-275 <BEV>
A:Cross-references: UNIPROT:Q5SUR3; UNIPARC:UPI00000822F; EMBL:AL035394
A:Experimental source: cultivar Columbia; BAC clone F9D16
C:Genetics:
A:Gene: CESP:T05595
A:Map position: 4
A:Introns: 89/1; 149/2; 196/3; 220/1
A>Note: F9D16.100
Query Match 43.7%; Score 76.5; DB 2; Length 275;
Best Local Similarity 40.5%; Pred. No. 0.059;
Matches 15; Conservative 9; Mismatches 10; Indels 3; Gaps 1;
```

QY 2 KPAVL---MWVTVVGVLFNGTLTLILALISLSPV 35
 DB 193 KFLIAIAGLWLSILGCGCFNLTLAYIALVLLFTVPL 229

RESULT 8
 A:Accession: AD1561
 B. subtilis YoaT protein homolog lin1029 [imported] - Listeria innocua (strain Clip11262)
 C:Species: Listeria innocua
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 12-Jul-2004
 C:Accession: AD1561
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, R.; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AD1561
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-267 <GLA>
 A:Cross-references: UNIPROT:Q92CZ2; UNIPARC:UPI00000CC42B; GB:AL592022; PIDN:CAC96260.1
 A:Experimental source: strain Clip11262
 C:Genetics:
 A:Gene: lin1029
 C:Superfamily: membrane protein

Query Match 42.6%; Score 74.5; DB 2; Length 267;
 Best Local Similarity 46.2%; Pred. No. 0.098;
 Matches 18; Conservative 5; Mismatches 13; Indels 3; Gaps 1;

QY 1 LKPAVLMMVTVVGVG---LFGNLTLLILALISLSPV 36
 DB 1 MKPFRLLMWFTWKQALCCLFPFGIIFISLALTKLIBPFI 39

RESULT 9
 A:Accession: AE1204
 B. subtilis YoaT protein homolog lmo1037 [imported] - Listeria monocytogenes (strain EGD)
 C:Species: Listeria monocytogenes
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 12-Jul-2004
 C:Accession: AE1204
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, R.; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AE1204
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-267 <GLA>
 A:Cross-references: UNIPROT:Q8Y880; UNIPARC:UPI0000054DF1; GB:NC_003210; PIDN:CAC99115.1
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: lmo1037
 C:Superfamily: membrane protein

Query Match 40.3%; Score 70.5; DB 2; Length 267;
 Best Local Similarity 43.6%; Pred. No. 0.29;
 Matches 17; Conservative 6; Mismatches 13; Indels 3; Gaps 1;

QY 1 LKPAVLMMVTVVGVG---LFGNLTLLILALISLSPV 36
 DB 1 MQPFRLLMWFTWKQALCCLFPFGIIFISLALTKLIBPFI 39

RESULT 10

TI3013
 hypothetical protein F8L21.10 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
 C:Accession: TI3013
 R:Payan, M.; Peters, S.A.; van Staveren, M.; Dickse, W.; Stiekema, W.; Bancroft, I.; Mew, J.
 submitted to the Protein Sequence Database, July 1999
 A:Reference number: Z17587
 A:Accession: TI3013
 A:Molecule type: DNA
 A:Residues: 1-271 <REV>
 A:Cross-references: UNIPROT:Q9SUT9; UNIPARC:UPI00000ACS1D; EMBL:AL096882; GSPDB:GN00062;
 A:Experimental source: cultivar Columbia; BAC clone F8L21
 C:Genetics:
 A:Gene: ATSP:F8L21.10
 A:Map position: 4
 A:Introns: 85/1; 145/2; 192/3; 216/1

Query Match 38.9%; Score 68; DB 2; Length 271;
 Best Local Similarity 37.9%; Pred. No. 0.58;
 Matches 11; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 7 MWVTVVGVLFNGTLTLILALISLSPV 35
 DB 197 LWVLSILGCGCYSLTLAYIALVLLFTVPL 225

RESULT 11
 E84899
 hypothetical protein At2g46170 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: E84899
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: E84899
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-255 <STO>
 A:Cross-references: UNIPROT:O82352; UNIPARC:UPI00000A0AB3; GB:AE002093; NID:g3702332; PII
 C:Genetics:
 A:Gene: At2g46170
 A:Map position: 2

Query Match 37.7%; Score 66; DB 2; Length 255;
 Best Local Similarity 33.3%; Pred. No. 0.96;
 Matches 12; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 LKPAVLMMVTVVGVLFNGTLTLILALISLSPV 36
 DB 174 LMVVVGLWITSVGVGNFNLTLVYICFVILHTVPL 209

RESULT 12
 A84527
 hypothetical protein At2g15280 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: A84527
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: A84527
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-183 <STO>

us-09-830-972a-2_copy_1090_1125.rpr

Tue Feb 21 15:13:28 2006

A:Cross-references: UNIPROT:Q9SHU8; UNIPARC:UPI00000A63C8; GB:AB002093; NID:G462633; PID:Q9SHU8
 C:Genetics:
 A:Gene: At2g15280
 A:Map position: 2

Query Match 35.4%; Score 62; DB 2; Length 183;
 Best Local Similarity 31.4%; Pred. No. 2.1;
 Matches 11; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 2 KEAVLMVFTVVGALFNGLTLLILALISLFSIPVI 36
 DB 103 RVSVLMTVSFGNLFNLTLVGLVLSLLPL 137

RESULT 13
 A10142
 Probable membrane protein YPO1163 [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: A10142
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: A10142
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-236 <KUR>
 A:Cross-references: UNIPROT:Q8ZGW1; UNIPARC:UPI00000DCA1F; GB:AL590842; PIDN:CAC90004.1;
 C:Genetics:
 A:Gene: YPO1163
 C:Superfamily: Escherichia coli ybhL protein

Query Match 35.1%; Score 61.5; DB 2; Length 236;
 Best Local Similarity 63.6%; Pred. No. 3;
 Matches 14; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 1 LKFAVLMVFTVVGAL-FNGLT 21
 DB 163 LKSPALMVMVTVIGLVFVGLT 184

RESULT 14
 S12619
 Na+-transporting two-sector ATPase (EC 3.6.3.15) [similarity] - Propionigenium modestum
 C:Species: Propionigenium modestum
 C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 31-Dec-2004
 C:Accession: S12619; S12611; S29035; S23334; S24367; S36000
 R:Kaim, G.; Ludwig, W.; Dimroth, P.; Schleifer, K.H.
 Nucleic Acids Res. 18, 6697, 1990
 A:Title: Sequence of subunits a and b of the sodium ion translocating adenosine triphosph
 A:Reference number: S12619; MUID:91067471; PMID:2174545
 A:Accession: S12619
 A:Molecule type: DNA
 A:Residues: 1-289 <KAI>
 A:Cross-references: UNIPROT:P21903; UNIPARC:UPI000012632F; EMBL:X54809; NID:G45607; PIDN:P21903
 R:Esser, U.; Krumholz, L.R.; Simoni, R.D.
 Nucleic Acids Res. 18, 5887, 1990
 A:Title: Nucleotide sequence of the F(0) subunits of the sodium dependent F(1)F(0) ATPase
 A:Reference number: S12611; MUID:91016937; PMID:2170948
 A:Accession: S12611
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-113, 'I', 115-289 <ESS>
 A:Cross-references: UNIPARC:UPI000016FD91; EMBL:X53960; NID:G45643; PIDN:CAA37911.1; PIDN:CAA37911.1
 R:Krumholz, L.R.; Esser, U.; Simoni, R.D.
 FEBS Microbiol. Lett. 91, 37-42, 1992
 A:Title: Characterization of the genes coding for the F(1)F(0) subunits of the sodium de
 A:Reference number: S29034
 A:Accession: S29035
 A:Molecule type: DNA

A:Residues: 1-113, 'I', 115-289 <KRU1>
 A:Cross-references: UNIPARC:UPI0000175ED5; EMBL:X58461
 R:Krumholz, L.R.
 submitted to the EMBL Data Library, March 1991
 A:Reference number: S23333
 A:Accession: S23334
 A:Molecule type: DNA
 A:Residues: 1-113, 'I', 115-289 <KRU2>
 A:Cross-references: UNIPARC:UPI000016FD91; EMBL:X58461; NID:G897797; PIDN:CAA41368.1; PIDN:CAA41368.1
 R:Kaim, G.; Ludwig, W.; Dimroth, P.; Schleifer, K.H.
 Eur. J. Biochem. 207, 463-470, 1992
 A:Title: Cloning, sequencing and in vivo expression of genes encoding the F(0) part of th
 A:Reference number: S24366; MUID:92339434; PMID:11386022
 A:Accession: S24367
 A:Molecule type: DNA
 A:Residues: 1-95, 'L', 97-157, 'T', 158-205, 'L', 207-224, 'F', 226-289 <KAW>
 A:Cross-references: UNIPARC:UPI0000175ED6; EMBL:X66102
 R:Ludwig, W.
 submitted to the EMBL Data Library, May 1992
 A:Reference number: S36000
 A:Accession: S36000
 A:Molecule type: DNA
 A:Residues: 1-289 <LUD>
 A:Cross-references: UNIPARC:UPI000012632F; EMBL:X66102; NID:G45599; PIDN:CAA46894.1; PID:CAA46894.1
 C:Genetics:
 A:Gene: uncB
 C:Superfamily: H(+)-transporting ATP synthase protein 6
 C:Keywords: ATP biosynthesis; blocked amino end; hydrolase; membrane-associated complex;

Query Match 34.9%; Score 61; DB 2; Length 289;
 Best Local Similarity 56.0%; Pred. No. 4.1;
 Matches 14; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 10 FTVVGALFNGLTLLILALISLFSIP 34
 DB 126 FTVIGTLF--LFLISNIVSFPPIP 148

RESULT 15
 D71112
 hypothetical protein PH0667 - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
 C:Accession: D71112
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A:Reference number: A71000; MUID:98344137; PMID:9679194
 A:Accession: D71112
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-413 <KAW>
 A:Cross-references: UNIPROT:O58400; UNIPARC:UPI0000062E95; GB:AP000003; NID:G3236130; PIDN:G3236130
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PH0667

Query Match 34.0%; Score 59.5; DB 2; Length 413;
 Best Local Similarity 38.7%; Pred. No. 8.5;
 Matches 12; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 2 KEAVLMVFTVVGALFNGLTLLILALISLFS 32
 DB 308 KLAILGYLTFTGVAV--ATTIIMALVSLLS 337

Search completed: February 17, 2006, 03:56:52
 Job time : 26.7778 secs

CC block the regeneration of the nervous central system in adults (By
CC similarity).
CC -|- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
CC similarity).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
CC membrane of the endoplasmic reticulum through 2 putative
CC transmembrane domains (By similarity).
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms may be produced;
CC Name=1;
CC
CC IsoId=Q9P72-1; Sequence=Displayed;
CC -|- SIMILARITY: Contains 1 reticulon domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF126337; AK08076.1; -; mRNA.
CC EMBL; AK003859; -; NOT ANNOTATED CDS; mRNA.
CC Ensembl; ENSMUSG0000020458; Mus musculus.
CC WGI; WGI-1915835; Rtn4
CC GO; GO:0042395; C:cell projection; IDA.
CC GO; GO:0043025; C:cell soma; IDA.
CC GO; GO:0005783; C:endoplasmic reticulum; IDA.
CC GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.
CC GO; GO:0005635; C:nuclear membrane; ISS.
CC GO; GO:0005225; P:protein binding; ISS.
CC GO; GO:0001825; P:angiogenesis; IMP.
CC GO; GO:0019967; P:negative regulation of anti-apoptosis; ISS.
CC GO; GO:0030517; P:negative regulation of axon extension; ISS.
CC GO; GO:0007399; P:neurogenesis; IDA.
CC InterPro; IPR003386; Reticulon; 1.
CC PANTHER; PTHR10994; Reticulon; 1.
CC Pfam; PF04593; Reticulon; 1.
CC PROSITE; PS50845; RETICULON; 1.
CC KW Alternative splicing; Endoplasmic reticulum; Transmembrane.
FT TOPO_DOM 1 25 Cytoplasmic (Potential).
FT TRANSMEM 26 50 Potential.
FT TOPO_DOM 51 137 Luminal (Potential).
FT TRANSMEM 138 162 Potential.
FT TOPO_DOM 163 199 Cytoplasmic (Potential).
FT DOMAIN 12 199 Reticulon.
FT SEQUENCE 199 AA; 22466 MW; 07BE5D580059ED9C CRC64;
Query Match 100.0%; Score 175; DB 1; Length 199;
Best Local Similarity 100.0%; Pred. No. 4.9e-12; Gaps 0;
Matches 36; Conservative 0; Mismatches 0; Indels 0;
Qy 1 LKFAVLWVFTYVGVGALFNGLTLLILALISLFSIPVI 36
Db 126 LKFAVLWVFTYVGVGALFNGLTLLILALISLFSIPVI 161
RESULT 2
Q78NS1 MOUSE PRELIMINARY; PRT; 199 AA.
AC Q78NS1;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE RTN4 (Reticulon 4).
GN Name=Rtn4; ORFNames=RP23-17605.4-009;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129SVCJ7, and 129/SvcJ7;
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

RA MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
RT human and mouse nogo/rtn4.";
RL J. Mol. Biol. 325:299-323 (2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129SVCJ7;
RA Van der Putten H., Mir A.;
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvcJ7;
RA Van der Putten H.;
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Kay M.;
RA Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY102286; AA073503.1; -; mRNA.
DR EMBL; AY102286; AA073503.1; -; Genomic DNA.
DR EMBL; AL929371; CA124272.1; -; Genomic DNA.
DR Ensembl; ENSMUSG0000020458; Mus musculus.
Query Match 100.0%; Score 175; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 4.9e-12; Gaps 0;
Matches 36; Conservative 0; Mismatches 0; Indels 0;
Qy 1 LKFAVLWVFTYVGVGALFNGLTLLILALISLFSIPVI 36
Db 126 LKFAVLWVFTYVGVGALFNGLTLLILALISLFSIPVI 161
RESULT 3
Q8BH78 MOUSE PRELIMINARY; PRT; 356 AA.
AC Q8BH78;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE RTN4 (Reticulon 4).
GN Name=Rtn4; ORFNames=RP23-17605.4-007;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvcJ7, and 129SVCJ7;
RA MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
RT human and mouse nogo/rtn4.";
RL J. Mol. Biol. 325:299-323 (2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvcJ7;
RA Van der Putten H.;
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129SVCJ7;
RA Van der Putten H., Mir A.;
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Kay M.;
RA Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY102286; AA073503.1; -; mRNA.
DR EMBL; AY102286; AA073503.1; -; Genomic DNA.
DR EMBL; AL929371; CA124272.1; -; Genomic DNA.
DR Ensembl; ENSMUSG0000020458; Mus musculus.

DR MGI:1915835; Rtn4.
 DR GO:0042995; C:cell projection; IDA.
 DR GO:0043025; C:cell soma; IDA.
 DR GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO:0005155; P:protein binding; IPI.
 DR GO:0001525; P:angiogenesis; IMP.
 DR GO:0007399; P:neurogenesis; IDA.
 DR InterPro: IPR003388; Reticulon.
 DR Pfam: PF02453; Reticulon; 1.
 DR PROSITE: PS50845; RETICULON; 1.
 SQ SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;
 Query Match 100.0%; Score 175; DB 2; Length 356;
 Best Local Similarity 100.0%; Pred. No. 7.5e-12;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
 Db 293 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 318
 RESULT 4
 ID Q8K3G7_MOUSE PRELIMINARY; PRT; 357 AA.
 AC Q8K3G7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Nogo-B.
 GN Name=Rtn4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c;
 RA Jin W., Li R., Long M., Shen J., Ju G.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY114153; AA077069.1; -; mRNA.
 DR MGI: MGI:1915835; Rtn4.
 DR GO:0042995; C:cell projection; IDA.
 DR GO:0043025; C:cell soma; IDA.
 DR GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO:0005155; P:protein binding; IPI.
 DR GO:0001525; P:angiogenesis; IMP.
 DR GO:0007399; P:neurogenesis; IDA.
 DR InterPro: IPR003388; Reticulon.
 DR Pfam: PF02453; Reticulon; 1.
 DR PROSITE: PS50845; RETICULON; 1.
 SQ SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;
 Query Match 100.0%; Score 175; DB 2; Length 357;
 Best Local Similarity 100.0%; Pred. No. 7.5e-12;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
 Db 284 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 319
 RESULT 5
 ID Q6IRL3_RAT PRELIMINARY; PRT; 360 AA.
 AC Q6IRL3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Rtn4 protein (Rtn4-B1).
 GN Name=Rtn4;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE
 RC TISSUE=Lung; 8257 Placenta;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg K.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wegner L., Shenmen C.W., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22715887; PubMed=12832288;
 RA Certle T., Klinger M., Stuermer C.A., Schwab M.E.;
 RT "A reticular rhapody: phylogenetic evolution and nomenclature of the
 Rtn/Nogo gene family.";
 RL PASEB J. 17:1238-1247(2003).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Placenta;
 RG NIH MGC Project;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC070879; AAH70879.1; -; mRNA.
 DR EMBL: AY164740; AAP47315.1; -; mRNA.
 DR EMBL: BC097936; AAH97936.1; -; mRNA.
 DR GO:0005783; C:endoplasmic reticulum; IEA.
 DR InterPro: IPR003388; Reticulon.
 DR Pfam: PF02453; Reticulon; 1.
 DR PROSITE: PS50845; RETICULON; 1.
 SQ SEQUENCE 360 AA; 38822 MW; 149714AD6C3D5A7 CRC64;
 Query Match 100.0%; Score 175; DB 2; Length 360;
 Best Local Similarity 100.0%; Pred. No. 7.6e-12;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
 Db 287 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 322
 RESULT 6
 ID Q8BHF5_MOUSE PRELIMINARY; PRT; 375 AA.
 AC Q8BHF5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Rtn4 (Reticulon 4).
 GN Name=Rtn4; ORFNames=RP23-17605.4-006;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/SVCJ7, and 129SVCJ7;
 RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
 RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
 RT "Genomic structure and functional characterisation of the promoters of
 human and mouse nogo/rtn4.";
 RL J. Mol. Biol. 325:299-323 (2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/SVCJ7;
 RX STRAIN=129/SVCJ7;
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129SVCJ7;
 RA Van der Putten H., Mir A.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Kay M.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AV102282; AM73504.1; -; mRNA.
 DR EMBL; AV102286; AM73509.1; -; Genomic DNA.
 DR EMBL; AL924371; CA124271.1; -; Genomic DNA.
 DR EMBL; EMBMSG0000020458; Mus musculus.
 DR MGI; MGI_1315835; Rtn4.
 DR GO; GO:0043299; C:cell projection; IDA.
 DR GO; GO:0043025; C:cell soma; IDA.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0005125; P:angiogenesis; IMP.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS00845; RETICULON; 1.
 DR SEQUENCE 375 AA; 40300 MW; 23D9EB19BE671AE6 CRC64;
 SQ

Query Match 100.0%; Score 175; DB 2; Length 375;
 Best Local Similarity 100.0%; Pred. No. 7.8e-12;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LKPAVLMVFTYVGVGALFNGLTLLILALISLFSIPVI 36
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 Db 302 LKPAVLMVFTYVGVGALFNGLTLLILALISLFSIPVI 337

RESULT 7

Q540J3 RAT
 ID Q540J3 RAT PRELIMINARY; PRT; 379 AA.
 AC Q540J3;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE RTN4-B2.
 GN Name=Rtn4;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=22715887; PubMed=12832288;
 RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
 RT "A reticular thapsody: phylogenetic evolution and nomenclature of the
 RTN/Nogo gene family.";
 RL PNAS 97:1238-1247 (2000).
 DR EMBL; AV164741; RAP47316.1; -; mRNA.
 DR SEQUENCE 379 AA; 40719 MW; 9F15AB942D36ED0F CRC64;
 SQ

Query Match 100.0%; Score 175; DB 2; Length 379;
 Best Local Similarity 100.0%; Pred. No. 7.8e-12;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LKPAVLMVFTYVGVGALFNGLTLLILALISLFSIPVI 36
 |||||
 Db 306 LKPAVLMVFTYVGVGALFNGLTLLILALISLFSIPVI 341

RESULT 8

Q80W95 MOUSE
 ID Q80W95 MOUSE PRELIMINARY; PRT; 578 AA.
 AC Q80W95;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nogo-A (Fragment).
 GN Name=Rtn4; Synonym=Nogo-A;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Tozaki H., Hirata T.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB073672; BAC75974.1; -; mRNA.
 DR MGI; MGI_1915835; Rtn4.
 DR GO; GO:0042995; C:cell projection; IDA.
 DR GO; GO:0043025; C:cell soma; IDA.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0005125; P:angiogenesis; IMP.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS00845; RETICULON; 1.
 DR NON-TER;
 DT SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;
 SQ

Query Match 100.0%; Score 175; DB 2; Length 578;
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LKPAVLMVFTYVGVGALFNGLTLLILALISLFSIPVI 36
 |||||
 Db 505 LKPAVLMVFTYVGVGALFNGLTLLILALISLFSIPVI 540

RESULT 9

Q8K290 MOUSE
 ID Q8K290 MOUSE PRELIMINARY; PRT; 639 AA.
 AC Q8K290;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Rtn4 protein.
 GN Name=Rtn4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TSSUE=Mammary tumor. C3;
 RX MEDLINE=12477932; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 KLautner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,


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DR GO: 0043025; C:cell soma; IDA.
DR GO: 0005783; C:endoplasmic reticulum; IDA.
DR GO: 0005515; F:protein binding; IPI.
DR GO: 0001525; P:angiogenesis; IMP.
DR GO: 0007399; P:neurogenesis; IDA.
DR InterPro: IPR003388; Reticulon.
DR Pfam: PF02453; Reticulon; 1.
DR PROSITE: PS00845; RETICULON; 1.
DR SEQUENCE 1162 AA; 126612 MW; 855697FBE11781F CRC64;

Query Match 100.0%; Score 175; DB 2; Length 1162;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGLFNGLTLLILALISLFSIPVI 36
      |||
DB 1089 LKFAVLMMVFTYVGLFNGLTLLILALISLFSIPVI 1124

RESULT 12
RTN4 RAT STANDARD; PRT: 1163 AA.
AC Q9JX11; Q9JX10; Q9R0D9; Q9WUE9; Q9WUFO;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foccen)
DE (Gluc4 vesicle 20 kDa protein).
GN Name=RTN4; Synonyms=Nogo;
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 3), AND PARTIAL PROTEIN SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte; DOI=10.1016/S0167-4889(99)00033-6;
RX MEDLINE=9249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6;
RA Morris N.J., Ross S.A., Neveu J.W., Lane W.S., Lienhard G.E.;
RT "Cloning and characterization of a 22 kDa protein from rat adipocytes:
a new member of the reticulon family.";
RL Biochim. Biophys. Acta 1450:68-76(1999).
[2]
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20129259; PubMed=10667796; DOI=10.1038/35000219;
RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
RA Spillmann A.A., Christ F., Schwab M.E.;
RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
antigen for monoclonal antibody IN-1.";
RL Nature 403:434-439(2000).
[3]
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 2 AND 4).
RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;
RA Ito T., Schwartz S.M.;
RT "Cloning of a member of the reticulon gene family in rat: one of two
minor splice variants.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
[4]
RN [4]
RP FUNCTION.
RX MEDLINE=20033691; PubMed=12037567; DOI=10.1038/417547a;
RA GrandPre T., Li S., Strittmatter S.M.;
RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
RL Nature 417:547-551(2002).
CC -1- FUNCTION: Potent neurite outgrowth inhibitor which may also help
block the regeneration of the nervous central system in adults (by
similarity).
CC -1- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (by
similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
membrane of the endoplasmic reticulum through 2 putative
transmembrane domains (by similarity).
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
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Q8K3G8_MOUSE
ID Q8K3G8_MOUSE PRELIMINARY; PRT; 1163 AA.
AC Q8K3G8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nogo-A.
GN Nogo-A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Jin W., Long M., Li R., Ju G.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY114152; AAM77068.1; -; mRNA.
DR MGI; MGI:1915835; Rtn4.
DR GO; GO:0043995; C:cell projection; IDA.
DR GO; GO:0043025; C:cell soma; IDA.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0001525; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1163 AA; 126690 MW; 6B5F362799417EA4 CRC64;
Query Match 100.0%; Score 175; DB 2; Length 1163;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
DB 1090 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1125
RESULT 14
QSDTK9_MOUSE
ID QSDTK9_MOUSE PRELIMINARY; PRT; 1245 AA.
AC QSDTK9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE MKTAA4153 protein (Fragment).
GN Name=Rtn4; Synonym=smKTA4153;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Fetal Brain;
RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Nagase T., Ohara O.,
RT Koga H.;
RL "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene.
RT The Complete Nucleotide Sequences of Mouse KIAA-homologous cDNAs
RT Identified by Screening of Terminal Sequences of cDNA Clones Randomly
RT Sampled from Size-Fractionated Libraries.",
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK220511; BAD90301.1; -; mRNA.
DR MGI; MGI:1915835; Rtn4.
DR GO; GO:0042995; C:cell projection; IDA.
DR GO; GO:0043025; C:cell soma; IDA.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0001525; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
FT NON_TER 1
SQ SEQUENCE 1245 AA; 135257 MW; 85460D746CE7F16C CRC64;
Query Match 100.0%; Score 175; DB 2; Length 1245;
Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
DB 1172 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1207
RESULT 15
Q53SV1_HUMAN
ID Q53SV1_HUMAN PRELIMINARY; PRT; 187 AA.
AC Q53SV1;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein RTN4 (Fragment).
GN Name=RTN4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Maupin R., Haakenson W., Boyer E., Kang K.;
RL "The sequence of Homo sapiens BAC clone Rp11-56013.",
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.H.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC013414; AAY24239.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 187 AA; 20936 MW; A161F7A143C4607C CRC64;
Query Match 99.4%; Score 174; DB 2; Length 187;
Best Local Similarity 97.2%; Pred. No. 6.1e-12;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
DB 114 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 149
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Job time : 165.444 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: February 17, 2006, 03:56:08 ; Search time 38.2222 Seconds
(without alignments)
77.869 Million cell updates/sec
Title: US-09-830-972A-2_COPY_1090_1125
Perfect score: 175
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database :
1: /cgn2_6/ptodata/1/iaa/5 COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/PTUS COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	174	99.4	1	US-08-700-607-1
2	174	99.4	2	US-09-949-016-9124
3	150	85.7	208	US-08-700-607-7
4	150	85.7	267	US-08-700-607-8
5	150	85.7	356	US-08-700-607-6
6	150	85.7	439	US-09-949-016-9180
7	150	85.7	776	US-08-700-607-5
8	150	85.7	776	US-09-949-016-6998
9	136	77.7	219	US-09-270-767-45132
10	131	74.9	92	US-09-149-476-411
11	131	74.9	168	US-09-149-476-563
12	131	74.9	192	US-09-949-016-8859
13	124	70.9	241	US-08-700-607-3
14	120	68.6	588	US-09-949-016-7290
15	61.5	35.1	242	US-09-489-039A-12517
16	60.5	34.6	117	US-08-973-068-5
17	59	33.7	289	US-09-540-236-2019
18	57.5	32.9	242	US-09-489-039A-13008
19	56	32.0	268	US-09-198-452A-121
20	56	32.0	349	US-09-438-185A-105
21	55.5	31.7	744	US-09-785-381-3
22	55.5	31.7	744	US-09-785-381-3
23	54.5	31.1	970	US-09-795-927-7
24	54	30.9	213	US-09-583-110-3395
25	54	30.9	342	US-09-134-001C-4190
26	54	30.9	363	US-09-248-796A-17364
27	54	30.9	470	US-09-543-681A-4625

Sequence 4234, Ap
Sequence 21088, A
Sequence 32657, A
Sequence 21625, A
Sequence 6126, Ap
Sequence 2594, Ap
Sequence 36, Appl
Sequence 692, Appl
Sequence 655, Appl
Sequence 29264, A
Sequence 4246, Ap
Sequence 5431, Ap
Sequence 16020, A
Sequence 5457, Ap
Sequence 9915, Ap
Sequence 4817, Ap
Sequence 2, Appl
Sequence 164, Appl

RESULT 1
US-08-700-607-1
Sequence 1, Application US/08700607
Patent No. 5858708
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-08-700-607-1
Query Match 99.4%; Score 174; DB 1; Length 199;
Best Local Similarity 97.2%; Pred. No. 6.1e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKPAVLMMVFTYVYGALFNGLTLLILALISLFSIPVI 36

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;
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307311
US-08-700-607-7

Query Match      85.7%; Score 150; DB 1; Length 208;
Best Local Similarity 72.2%; Pred. No. 7.9e-12;
Matches 26; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY      1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
DB      135 LKFAVLNMLLTIVGALFNGLTLLILMAVSMFTLPVV 170

RESULT 4
US-08-700-607-8
; Sequence 8, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 281046
US-08-700-607-8

Query Match      85.7%; Score 150; DB 1; Length 267;
Best Local Similarity 72.2%; Pred. No. 1e-11;
Matches 26; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY      1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
DB      126 LKFAVLNMLLTIVGALFNGLTLLILMAVSMFTLPVV 161

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; LENGTH: 201
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9124

Query Match      99.4%; Score 174; DB 2; Length 201;
Best Local Similarity 97.2%; Pred. No. 6.2e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
DB      128 LKFAVLNMLLTIVGALFNGLTLLILALISLFSVPVI 163

RESULT 3
US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
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RESULT 5
US-08-700-607-6
; Sequence 6, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307309
;
US-08-700-607-6
Query Match      85.7%; Score 150; DB 1; Length 356;
Best Local Similarity 72.2%; Pred. No. 1.4e-11;
Matches 26; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LKFAVLMMVPTVVGALFNGLTLLILALISLPSIPVI 36
Db      283 LKFAVLMMVPTVVGALFNGLTLLILALISLPSIPVI 318

RESULT 6
US-09-949-016-9180
; Sequence 9180, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 9180
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9180

Query Match      85.7%; Score 150; DB 2; Length 439;
Best Local Similarity 72.2%; Pred. No. 1.7e-11;
Matches 26; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LKFAVLMMVPTVVGALFNGLTLLILALISLPSIPVI 36
Db      366 LKFAVLMMVPTVVGALFNGLTLLILALISLPSIPVI 401

RESULT 7
US-08-700-607-5
; Sequence 5, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
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US-08-700-607-5
Query Match      85.7%; Score 150; DB 1; Length 776;
Best Local Similarity 72.2%; Pred. No. 3.2e-11;
Matches 26; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LKFAVLMMVPTVVGALFNGLTLLILALISLPSIPVI 36
Db      703 LKFAVLMMVPTVVGALFNGLTLLILALISLPSIPVI 738

RESULT 8
US-09-949-016-6998
; Sequence 6998, Application US/09949016
; Patent No. 6812339
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us-09-830-972a-2_copy_1090_1125.ra1

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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6998
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6998

Query Match      85.7%; Score 150; DB 2; Length 776;
Best Local Similarity 72.2%; Pred. No. 3.2e-11;
Matches 26; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY      1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
       703 LKFAVLMMLTITVGALFNGLTLLILMAVSMFTLPVV 738

Db

RESULT 9
US-09-270-767-45132
; Sequence 45132, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1997-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45132
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-45132

Query Match      77.7%; Score 136; DB 2; Length 219;
Best Local Similarity 63.9%; Pred. No. 5.2e-10;
Matches 23; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY      1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
       137 IKFGVILMVFTYVGAWFNGMTLVILAFVSLTLPKV 172

Db

RESULT 10
US-09-149-476-411
; Sequence 411, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313

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Tue Feb 21 15:13:27 2006

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 74.9%; Score 131; DB 2; Length 168;
Best Local Similarity 63.9%; Pred. No. 1.7e-09;
Matches 23; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 LKFAVLMVFTYVGVNGTLTLLALISLFSIPVI 36
DB 93 LKLAFFMMLTYVGVNGITLLILAEILFSVPV 128

RESULT 12
US-09-949-016-8859
; Sequence 8859, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8859
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8859

Query Match 74.9%; Score 131; DB 2; Length 192;
Best Local Similarity 63.9%; Pred. No. 2e-09;
Matches 23; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 LKFAVLMVFTYVGVNGTLTLLALISLFSIPVI 36

DB 118 LKLAFFMMLTYVGVNGITLLILAEILFSVPV 153

RESULT 13
US-08-700-607-3
; Sequence 5, Application US/08700607
; Patent No. 5856789
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Yang, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: TFF1NOB01
; CLONE: 31870
US-08-700-607-3

Query Match 70.9%; Score 124; DB 1; Length 241;
Best Local Similarity 61.1%; Pred. No. 2e-08;
Matches 22; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 LKFAVLMVFTYVGVNGITLLILAEILFSIPVI 36
DB 162 LKLAFFMMLTYVGVNGITLLILAEILFSVPV 197

RESULT 14
US-09-949-016-7290
; Sequence 7290, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03

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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO: 7230
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7290

Query Match          68.6%;   Score 120;   DB 2;   Length 588;
Best Local Similarity 61.1%;   Pred No. 1,7e-07;
Matches 22; Conservative          9; Mismatches 5; Indels 0; Gaps 0;

QY      1 LKFAVLMMWVTVYVGALPFGNLGLLILALISLSPVPI 36
DB      502 LKALLPYLTFVGAIFNGTLILGVIGLFTIPLL 537

RESULT 15
US-09-489-039A-12517
; Sequence 12517, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12517
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12517

Query Match          35.1%;   Score 61.5;   DB 2;   Length 242;
Best Local Similarity 44.7%;   Pred. No. 2.2;
Matches 17; Conservative          4; Mismatches 8; Indels 9; Gaps 2;

QY      6 LMWV--FTYVGALP-----NGLTLILALISLFSIP 34
DB      188 LLWVLLFTYAGYLFGLPVVQENKLIVAVIIVLSVLP 225

Search completed: February 17, 2006, 03:58:22
Job time : 39.2222 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 17, 2006, 03:57:08 ; Search time 130.222 Seconds
(without alignments)
115.509 Million cell updates/sec

Title: US-09-830-972A-2_COPY_1090_1125
Perfect score: 175
Sequence: 1 LKFAVLMWVFTYVGVGLFNGLTLLILALISLFSIPVI 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	175	100.0	199	3	US-09-893-348-21
2	175	100.0	199	5	US-10-810-653-21
3	175	100.0	360	3	US-09-893-348-20
4	175	100.0	360	5	US-10-810-653-20
5	175	100.0	379	4	US-10-205-194-164
6	175	100.0	1162	4	US-10-633-423-10
7	175	100.0	1162	4	US-10-427-741-10
8	175	100.0	1163	3	US-09-893-348-18
9	175	100.0	1163	4	US-10-267-502-431
10	175	100.0	1163	5	US-10-810-653-18
11	174	99.4	175	6	US-11-111-953-184
12	174	99.4	199	3	US-09-893-348-25
13	174	99.4	199	3	US-09-978-360A-467
14	174	99.4	199	4	US-10-660-946-1
15	174	99.4	199	4	US-10-408-967-9
16	174	99.4	199	5	US-10-810-653-25
17	174	99.4	199	6	US-11-111-953-615
18	174	99.4	201	6	US-11-111-953-619
19	174	99.4	373	3	US-09-789-386-6
20	174	99.4	373	3	US-09-765-205-6
21	174	99.4	373	3	US-09-893-348-24
22	174	99.4	373	4	US-10-060-036-72
23	174	99.4	373	4	US-10-408-967-8
24	174	99.4	373	4	US-10-466-258-4
25	174	99.4	373	4	US-10-466-391A-4
26	174	99.4	373	5	US-10-810-653-24
27	174	99.4	373	5	US-10-347-669-6

28	174	99.4	1192	3	US-09-789-386-2
29	174	99.4	1192	3	US-09-758-140-6
30	174	99.4	1192	3	US-09-893-348-23
31	174	99.4	1192	3	US-09-972-599A-6
32	174	99.4	1192	4	US-10-060-036-71
33	174	99.4	1192	4	US-10-408-967-7
34	174	99.4	1192	4	US-10-267-502-429
35	174	99.4	1192	4	US-10-327-213-9
36	174	99.4	1192	4	US-10-466-258-9
37	174	99.4	1192	4	US-10-466-391A-9
38	174	99.4	1192	5	US-10-810-653-23
39	174	99.4	1192	6	US-11-090-836-3
40	174	99.4	1192	6	US-11-090-846-3
41	174	99.4	1192	6	US-11-090-847-3
42	150	85.7	208	4	US-10-660-946-7
43	150	85.7	267	4	US-10-205-194-127
44	150	85.7	267	4	US-10-660-946-8
45	150	85.7	356	4	US-10-660-946-6

ALIGNMENTS

RESULT 1
US-09-893-348-21
; Sequence 21, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ-2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-21

Query Match 100.0% Score 175; DB 3; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.6e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKFAVLMWVFTYVGVGLFNGLTLLILALISLFSIPVI 36
Db 126 LKFAVLMWVFTYVGVGLFNGLTLLILALISLFSIPVI 161

RESULT 2
US-10-810-653-21
; Sequence 21, Application US/10810653
; Publication No. US20040253218A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

us-09-830-972a-2_copy_1090_1125.rapbm

Tue Feb 21 15:13:28 2006

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; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/10/810,653
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US/09/893,348
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-810-653-21
Query Match 100.0%; Score 175; DB 5; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.6e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
Db 126 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 161

RESULT 3
US-09-893-348-20
; Sequence 20, Application US/09893348
; Patent No. US200207493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-20
Query Match 100.0%; Score 175; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 3e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
Db 287 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 322

RESULT 4
US-10-810-653-20
; Sequence 20, Application US/10810653
; Publication No. US20040253218A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-20
Query Match 100.0%; Score 175; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 3e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
Db 287 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 322

RESULT 5
US-10-205-194-164
; Sequence 164, Application US/10205194
; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pincock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Footcan-m2 reticulon
US-10-205-194-164
Query Match 100.0%; Score 175; DB 4; Length 379;
Best Local Similarity 100.0%; Pred. No. 3.1e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
Db 306 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 341

RESULT 6
US-10-810-653-20
; Sequence 20, Application US/10810653
; Publication No. US20040253218A1
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Tue Feb 21 15:13:28 2006

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US-10-633-423-10
; Sequence 10, Application US/10633423
; Publication No. US20040191240A1
; GENERAL INFORMATION:
; APPLICANT: Tohyama, Masaya
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
; FILE REFERENCE: 59150-8023.US00
; CURRENT APPLICATION NUMBER: US/10/633,423
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: US 10/427,741
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: JP 2003-92923
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-633-423-10

Query Match      100.0%; Score 175; DB 4; Length 1162;
Best Local Similarity 100.0%; Pred. No. 9.7e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
DB 1089 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1124

RESULT 7
US-10-427-741-10
; Sequence 10, Application US/10427741
; Publication No. US20040191291A1
; GENERAL INFORMATION:
; APPLICANT: Tohyama, Masaya
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
; FILE REFERENCE: 59150-8023
; CURRENT APPLICATION NUMBER: US/10/427,741
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: JP 2003-92923
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-427-741-10

Query Match      100.0%; Score 175; DB 4; Length 1162;
Best Local Similarity 100.0%; Pred. No. 9.7e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
DB 1089 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1124

RESULT 8
US-09-893-348-18
; Sequence 18, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ=2A

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; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: FC/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-18

Query Match      100.0%; Score 175; DB 3; Length 1163;
Best Local Similarity 100.0%; Pred. No. 9.7e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
DB 1090 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1125

RESULT 9
US-10-267-502-431
; Sequence 431, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSO-07415
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 431
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-267-502-431

Query Match      100.0%; Score 175; DB 4; Length 1163;
Best Local Similarity 100.0%; Pred. No. 9.7e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
DB 1090 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1125

RESULT 10
US-10-810-653-18
; Sequence 18, Application US/10810653
; Publication No. US20040253218A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/10/810,653
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US/09/893,348
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19

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PRIOR APPLICATION NUMBER: US 09/247,155
PRIOR FILING DATE: 1999-02-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 810
SOFTWARE: Patent.pm
SEQ ID NO 467
LENGTH: 199
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: SIGNAL
LOCATION: -42..-1
US-09-978-360A-467

Query Match 99.4%; Score 174; DB 3; Length 199;
Best Local Similarity 97.2%; Pred. No. 2.2e-14;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPAVLMMVFTYVGVGALFNGLTLLILALISLFSIPVI 36
DB 126 LKPAVLMMVFTYVGVGALFNGLTLLILALISLFSVPVI 161

RESULT 14
US-10-660-946-1
Sequence 1, Application US/10660946
Publication No. US20040063131A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Au-Young, Janice
Goli, Surya K.
Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/660,946
FILING DATE: 12-Sep-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/228,213A
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/700,607
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-0555
TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: Consensus
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-660-946-1

Query Match 99.4%; Score 174; DB 4; Length 199;
Best Local Similarity 97.2%; Pred. No. 2.2e-14;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPAVLMMVFTYVGVGALFNGLTLLILALISLFSIPVI 36
DB 126 LKPAVLMMVFTYVGVGALFNGLTLLILALISLFSVPVI 161

RESULT 15
US-10-408-967-9
Sequence 9, Application US/10408967
Publication No. US20040063161A1
GENERAL INFORMATION:
APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Yan, Yifeng
APPLICANT: Lu, Yifeng
TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
FILE REFERENCE: 00925
CURRENT APPLICATION NUMBER: US/10/408,967
CURRENT FILING DATE: 2003-04-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 199
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-967-9

Query Match 99.4%; Score 174; DB 4; Length 199;
Best Local Similarity 97.2%; Pred. No. 2.2e-14;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPAVLMMVFTYVGVGALFNGLTLLILALISLFSIPVI 36
DB 126 LKPAVLMMVFTYVGVGALFNGLTLLILALISLFSVPVI 161

Search completed: February 17, 2006, 04:03:21
Job time : 131.222 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 17, 2006, 03:58:38 ; Search time 11.5556 Seconds
(without alignments)
44.284 Million cell updates/sec

Title: US-09-830-972A-2_COPY_1090_1125
Perfect score: 175
Sequence: 1 LKFAVLMMVFTYVGVGLFGLTLILALISLFSIPVI 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB_PEP.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB_PEP.*
4: /cgn2_6/ptodata/1/pubpaa/PCRT_NEW_PUB_PEP.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB_PEP.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB_PEP.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB_PEP.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	175	100.0	186	7	US-11-044-899-25
2	175	100.0	1163	7	US-11-044-899-2
3	175	100.0	1163	7	US-11-044-899-30
4	174	99.4	186	7	US-11-044-899-24
5	174	99.4	199	5	US-09-378-360A-167
6	174	99.4	414	6	US-10-821-234-1170
7	174	99.4	1178	7	US-11-044-899-23
8	152	86.9	186	7	US-11-044-899-23
9	150	85.7	186	7	US-11-044-899-21
10	150	85.7	186	7	US-11-044-899-22
11	97	55.4	194	7	US-11-044-899-26
12	63	36.0	150	7	US-11-044-899-27
13	53	30.3	769	6	US-10-505-263-81
14	51.5	29.4	778	6	US-10-505-263-81
15	50	28.6	252	6	US-10-055-877-107
16	50	28.6	276	6	US-10-055-877-111
17	50	28.6	276	6	US-10-055-877-115
18	50	28.6	355	7	US-11-218-281-26
19	50	28.6	552	6	US-10-055-877-305
20	50	28.6	664	6	US-10-624-932-10
21	50	28.6	684	6	US-10-055-877-105
22	50	28.6	704	6	US-10-055-877-113
23	50	28.6	743	6	US-10-055-877-109
24	49	28.0	400	7	US-11-329-371-123
25	49	28.0	400	7	US-11-329-371-123

26	49	28.0	424	7	US-11-229-371-113
27	49	28.0	424	7	US-11-228-923-113
28	49	28.0	664	6	US-10-055-877-306
29	49	28.0	664	6	US-10-055-877-307
30	47.5	27.1	315	7	US-11-044-347B-2
31	47.5	27.1	395	7	US-11-074-176-188
32	47.5	27.1	4473	6	US-10-895-064-460
33	47	26.9	319	6	US-10-873-528-44
34	47	26.9	431	6	US-10-793-626-5566
35	46.5	26.6	181	6	US-10-793-626-1842
36	46.5	26.6	288	7	US-11-098-686-10850
37	46.5	26.6	530	6	US-10-055-877-316
38	46	26.3	229	6	US-10-873-528-131
39	46	26.3	341	7	US-11-082-389-18
40	46	26.3	407	7	US-11-166-412-57
41	46	26.3	529	7	US-11-166-412-58
42	46	26.3	546	7	US-11-166-412-59
43	45.5	26.0	196	6	US-10-793-626-2584
44	45.5	26.0	336	6	US-10-793-626-1858
45	45.5	26.0	337	6	US-10-793-626-444

ALIGNMENTS

RESULT 1
US-11-044-899-25
; Sequence 25, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; APPLICANT: Chen, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044, 899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830, 972
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107, 446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Rattus sp.
US-11-044-899-25

Query Match 100.0%; Score 175; DB 7; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGVGLFGLTLILALISLFSIPVI 36
DB 113 LKFAVLMMVFTYVGVGLFGLTLILALISLFSIPVI 148

RESULT 2
US-11-044-899-2
; Sequence 2, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; APPLICANT: Chen, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044, 899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830, 972

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; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus sp.
US-11-044-899-2

Query Match          100.0%; Score 175; DB 7; Length 1163;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
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DB 1090 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1125

RESULT 3
US-11-044-899-30
; Sequence 30, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Chen, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: US/11/044,899
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus sp.
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Xaa = any amino acid
US-11-044-899-30

Query Match          100.0%; Score 175; DB 7; Length 1163;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
   |||||
DB 1090 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1125

RESULT 4
US-11-044-899-24
; Sequence 24, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: US/11/044,899
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus sp.
US-11-044-899-24

Query Match          99.4%; Score 174; DB 5; Length 199;
Best Local Similarity 97.2%; Pred. No. 2.5e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
   |||||
DB 113 LKFAVLMMVFTYVGALFNGLTLLILALISLFSVPVI 148

RESULT 5
US-09-978-360A-467
; Sequence 467, Application US/0978360A
; Publication No. US20060009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclozet, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.USA.CIP
; CURRENT FILING DATE: 2001-10-15
; CURRENT APPLICATION NUMBER: US/09/978,360A
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 467
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -42...-1
US-09-978-360A-467

Query Match          99.4%; Score 174; DB 5; Length 199;
Best Local Similarity 97.2%; Pred. No. 2.5e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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RESULT 10
US-11-044-899-22
; Sequence 22, Application US/11044899
; Publication NO. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044,899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830,972
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Rattus sp.
US-11-044-899-22

Query Match      85.7%; Score 150; DB 7; Length 186;
Best Local Similarity 72.2%; Pred. No. 2.4e-12;
Matches 26; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
Db      113 LKFAVLMWLTYYGALFNGLTLLILMAVSMFTLPVV 148

RESULT 11
US-11-044-899-26
; Sequence 26, Application US/11044899
; Publication NO. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044,899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830,972
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 194
; TYPE: PRT
; ORGANISM: C. elegans
US-11-044-899-26

Query Match      55.4%; Score 97; DB 7; Length 194;
Best Local Similarity 41.7%; Pred. No. 1.2e-05;
Matches 15; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Qy      1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
Db      113 IKFGLVLSLTIIASWFSGFTLAILGLGVFSVPKV 148

RESULT 12
US-11-044-899-27
; Sequence 27, Application US/11044899
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; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044,899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830,972
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 150
; TYPE: PRT
; ORGANISM: D. melanogaster
US-11-044-899-27

Query Match      36.0%; Score 63; DB 7; Length 150;
Best Local Similarity 51.9%; Pred. No. 0.18;
Matches 14; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy      1 LKFAVLMWVFTYVGALFNGLTLLILAL 27
Db      114 LKFLVLLCGINLLGDCFNGLTLLIFGM 140

RESULT 13
US-10-505-263-83
; Sequence 83, Application US/10505263
; Publication NO. US20060014940A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Case Western Reserve University
; APPLICANT: The Brigham and Women's Hospital, Inc.
; APPLICANT: Mount, David B
; APPLICANT: Romero, Michael
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF SLC26A6, SLC26A1, and SLC26A2
; FILE REFERENCE: 1242/50/2 PCT/US
; CURRENT APPLICATION NUMBER: US/10/505,263
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US 60/360,275
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US03/06469
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 83
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-505-263-83

Query Match      30.3%; Score 53; DB 6; Length 769;
Best Local Similarity 44.0%; Pred. No. 16;
Matches 11; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy      2 KFAVLMWVFTYVGALFNGLTLLILA 26
Db      460 RWDVAVWFTCVSAIILGLDLGLLA 484

RESULT 14
US-10-505-263-81
; Sequence 81, Application US/10505263
; Publication NO. US20060014940A1
; GENERAL INFORMATION:
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us-09-830-972a-2_copy_1090_1125.rapbn

Tue Feb 21 15:13:28 2006

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; APPLICANT: Vanderbilt University
; APPLICANT: Case Western Reserve University
; APPLICANT: The Brigham and Women's Hospital, Inc.
; APPLICANT: Mount, David B
; APPLICANT: Romero, Michael
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF SLC26A6, SLC26A1, and SLC26A2
; FILE REFERENCE: 1242/50/2 PCT/US
; CURRENT APPLICATION NUMBER: US/10/505,263
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US 60/360,275
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US03/06469
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 778
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-505-263-81

Query Match      29.4%; Score 51.5; DB 6; Length 778;
Best Local Similarity 37.1%; Pred. No.25;
Matches 13; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

QY 2 KFAVLMMVFTYVGVGALFNGTLTLLIALISLFSIPVI 36
DB 471 KMSVINVFTCIASILLGLDGLLAGL-LFGLVTI 504

RESULT 15
US-10-055-877-107
; Sequence 107, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eichen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shanket, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23

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; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-055-877-107

Query Match      28.6%; Score 50; DB 6; Length 252;
Best Local Similarity 30.8%; Pred. No.13;
Matches 8; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 10 FTVGVGALFNGTLTLLIALISLFSIPV 35
DB 101 YLYVFAILLGLTAIVIVIVSLCTPI 126

Search completed: February 17, 2006, 04:03:52
Job time : 12.5556 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 17, 2006, 03:57:08 ; Search time 97.6667 Seconds
(without alignments)
115.509 Million cell updates/sec

Title: US-09-830-972A-2_COPY_31_57
Perfect score: 139
Sequence: 1 EPEDEDEDEDEDEDEDELEVL 27
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	139	100.0	360	3	US-09-893-348-20 Sequence 20, Appl
2	139	100.0	360	5	US-10-810-653-20 Sequence 20, Appl
3	139	100.0	379	4	US-10-205-194-164 Sequence 164, Appl
4	139	100.0	1163	3	US-09-893-348-18 Sequence 18, Appl
5	119.5	86.0	1162	4	US-10-810-653-18 Sequence 18, Appl
6	119.5	86.0	1162	4	US-10-633-423-10 Sequence 10, Appl
7	119.5	86.0	1162	4	US-10-427-741-10 Sequence 10, Appl
8	119.5	86.0	1163	4	US-10-267-502-431 Sequence 431, Appl
9	111.5	80.2	373	3	US-09-789-386-6 Sequence 6, Appl
10	111.5	80.2	373	3	US-09-789-386-6 Sequence 6, Appl
11	111.5	80.2	373	3	US-09-893-348-24 Sequence 24, Appl
12	111.5	80.2	373	3	US-10-060-036-72 Sequence 72, Appl
13	111.5	80.2	373	4	US-10-408-967-8 Sequence 8, Appl
14	111.5	80.2	373	4	US-10-466-258-4 Sequence 4, Appl
15	111.5	80.2	373	4	US-10-466-391A-4 Sequence 4, Appl
16	111.5	80.2	373	5	US-10-810-653-24 Sequence 24, Appl
17	111.5	80.2	373	5	US-10-347-669-6 Sequence 6, Appl
18	111.5	80.2	1192	3	US-09-789-386-2 Sequence 2, Appl
19	111.5	80.2	1192	3	US-09-758-140-6 Sequence 6, Appl
20	111.5	80.2	1192	3	US-09-893-348-23 Sequence 23, Appl
21	111.5	80.2	1192	3	US-09-972-599A-6 Sequence 6, Appl
22	111.5	80.2	1192	4	US-10-060-036-71 Sequence 71, Appl
23	111.5	80.2	1192	4	US-10-408-967-7 Sequence 7, Appl
24	111.5	80.2	1192	4	US-10-267-502-429 Sequence 429, Appl
25	111.5	80.2	1192	4	US-10-327-213-9 Sequence 9, Appl
26	111.5	80.2	1192	4	US-10-466-258-9 Sequence 9, Appl
27	111.5	80.2	1192	4	US-10-466-391A-9 Sequence 9, Appl

28	111.5	80.2	1192	5	US-10-810-653-23 Sequence 23, Appl
29	111.5	80.2	1192	6	US-11-090-836-3 Sequence 3, Appl
30	111.5	80.2	1192	6	US-11-090-846-3 Sequence 3, Appl
31	111.5	80.2	1192	6	US-11-090-847-3 Sequence 3, Appl
32	99.5	71.6	306	4	US-10-437-155-242884 Sequence 197583
33	97	69.8	51	4	US-10-423-161A-2 Sequence 242884
34	97	69.8	208	3	US-09-214-881A-2 Sequence 2, Appl
35	97	69.8	208	5	US-10-728-195-2 Sequence 2, Appl
36	97	69.8	209	4	US-10-147-447-3 Sequence 3, Appl
37	97	69.8	209	4	US-10-300-072-3 Sequence 3, Appl
38	97	69.8	209	4	US-10-170-385-385 Sequence 385, App
39	97	69.8	209	4	US-10-456-949-3 Sequence 3, Appl
40	97	69.8	209	4	US-10-456-947-3 Sequence 3, Appl
41	97	69.8	209	4	US-10-718-495-3 Sequence 3, Appl
42	97	69.8	209	4	US-10-717-984-3 Sequence 3, Appl
43	97	69.8	209	5	US-10-733-878-493 Sequence 493, App
44	97	69.8	209	5	US-10-938-932-54 Sequence 54, Appl
45	97	69.8	244	4	US-10-264-049-3144 Sequence 3144, Ap

ALIGNMENTS

RESULT 1
US-09-893-348-20
; Sequence 20, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSNEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ#21
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-20

Query Match 100.0%; Score 139; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDELEVL 27
DB 31 EPEDEDEDEDEDEDELEVL 57

RESULT 2
US-10-810-653-20
; Sequence 20, Application US/10810653
; Publication No. US2004025318A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSNEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES


```
US-10-633-423-10
; Sequence 10, Application US/10633423
; Publication No. US20040191240A1
; GENERAL INFORMATION:
; APPLICANT: Tohyama, Masaya
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
; FILE REFERENCE: 59150-8023.US00
; CURRENT APPLICATION NUMBER: US/10/633,423
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: US 10/427,741
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: JP 2003-92923
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-633-423-10
Query Match      86.0%; Score 119.5; DB 4; Length 1162;
Best Local Similarity 92.6%; Pred. No. 0.00061;
Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPDEDEDEDEDEDEDEDEDEDELEVL 27
Db 31 EPDEDEDEDEE-EEDEDEDELEVL 56

RESULT 7
US-10-427-741-10
; Sequence 10, Application US/10427741
; Publication No. US20040191291A1
; GENERAL INFORMATION:
; APPLICANT: Tohyama, Masaya
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
; FILE REFERENCE: 59150-8023
; CURRENT APPLICATION NUMBER: US/10/427,741
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: JP 2003-92923
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-427-741-10
Query Match      86.0%; Score 119.5; DB 4; Length 1162;
Best Local Similarity 92.6%; Pred. No. 0.00061;
Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPDEDEDEDEDEDEDEDEDEDELEVL 27
Db 31 EPDEDEDEDEE-EEDEDEDELEVL 56

RESULT 8
US-10-267-502-431
; Sequence 431, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
US-10-267-502-431
Query Match      86.0%; Score 119.5; DB 4; Length 1163;
Best Local Similarity 92.6%; Pred. No. 0.00061;
Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPDEDEDEDEDEDEDEDEDEDELEVL 27
Db 31 EPDEDEDEDEE-EEDEDEDELEVL 56

RESULT 9
US-09-789-386-6
; Sequence 6, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-6
Query Match      80.2%; Score 111.5; DB 3; Length 373;
Best Local Similarity 85.2%; Pred. No. 0.0013;
Matches 23; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPDEDEDEDEDEDEDEDEDEDELEVL 27
Db 30 EPDEDEE-EEDEDEDEDEDELEVL 55

RESULT 10
US-09-765-205-6
; Sequence 6, Application US/09765205
; Patent No. US20020034800A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: human
US-09-765-205-6
Query Match      80.2%; Score 111.5; DB 3; Length 373;
Best Local Similarity 85.2%; Pred. No. 0.0013;
Matches 23; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
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Qy 1 EPEDDEEEEEEDEEDEDLEELVL 27
| | | | | : | | | | |
Dd 30 EPEDG-EEEEEEDEPEDELLELVL 55

```

RESULT 11
US-09-893-348-24
; Sequence 24, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BERSMAN, Pierre
; APPLICANT: MOSONOGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ-2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-24

```

RESULT 12
US-10-060-036-72
; Sequence 72, Application US/10060036

```
Qy      1 EPEDEEEEEEEDDEDLEELVL 27  
        ||||| ||||| :|||||  
Db     30 EPEDDE-EEEEEEEDDEDLEELVL 55
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```

RESULT 13
US-10-408-967-8
; Sequence 8, Application US/10408967
; Publication NO. US20040063161A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Yan, Riqiang
; APPLICANT: Lu, Yifeng
; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
; FILE REFERENCE: 00925
; CURRENT APPLICATION NUMBER: US/10/408,967
; CURRENT FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-967-8

Query Match      80.2%; Score 111.5; DB 4; Length 373;
Best Local Similarity 85.2%; Pred. NO. 0.0013;
Matches 23; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy      1 EPEDSEDEEEDEDEDEDEDELEVL 27
          ||||| ||||| :||| |||||
Db      30 EPEDSE-EEEEEDEDEDEDELEVL 55

```

```

RESULT 14
US-10-466-258-4
; Sequence 4, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
; CURRENT APPLICATION NUMBER: US/10/466,258
; CURRENT FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-466-258-4

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RESULT 15
US-10-466-391A-4
sequence 4, Application US/10466391A
Publication NO: US201040146953A1
ORIGINATOR: GLOBO GROUP LIMITED
APPLICANT: GLOBO GROUP LIMITED
TITLE OF INVENTION: ASSAY
FILE REFERENCE: P80966 GCW
CURRENT APPLICATION NUMBER: US/10/466,391A
CURRENT FILING DATE: 2003-07-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 4
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-466-391A-4

Query Match      80.2%; Score 111.5; DB 4; Length 373;
Best Local Similarity 85.2%; Pred. No. 0.0013;
Matches 23; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY      1 EPEDDEDEDEDEDEDEDEDEDELEVL 27
        ||||| ||||| :|||
Db      30 EPEDDE-EEEEDEDEDEDELEVL 55

Search completed: February 17, 2006, 04:03:20
Job time : 97.6667 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 17, 2006, 03:42:53 ; Search time 126.333 Seconds
(without alignments)
93.904 Million cell updates/sec

Title: US-09-830-972A-2_COPY_31_57
Perfect score: 139
Sequence: 1 EPDEDEDEDEDEDEDEDELEVL 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	100.0	171	3	Aay71561 Rat Nogo
2	139	100.0	359	3	Aay71558 Rat Nogo
3	139	100.0	360	3	Aay71383 Rat neuro
4	139	100.0	360	5	Abb81076 Rat neuro
5	139	100.0	361	3	Aay71385 Alternati
6	139	100.0	379	7	Adb85283 Rat foore
7	139	100.0	974	3	Aay71560 Rat Nogo
8	139	100.0	1162	3	Aay71557 Rat neuro
9	139	100.0	1163	3	Aay71310 Rat neuro
10	139	100.0	1163	3	Aay71384 Alternati
11	139	100.0	1163	5	Abb81074 Rat neuro
12	139	100.0	1163	8	Ado26399 Rat trunc
13	139	100.0	1163	8	Adp45572 Rat NogoA
14	139	100.0	1163	9	Adz07609 Rat NogoA
15	119.5	86.0	1162	8	Adt89537 Mus muscu
16	119.5	86.0	1162	8	Adt89537 Mus muscu
17	119.5	86.0	1163	8	Ado08105 Mouse pol
18	111.5	80.2	68	3	Agd02223 Human sec
19	111.5	80.2	185	8	Adq16418 Nucleotid
20	111.5	80.2	284	3	Aay95030 Human clo
21	111.5	80.2	360	4	Aae03987 Human gen
22	111.5	80.2	373	3	Aay53624 A bone na
23	111.5	80.2	373	3	Aay56969 Human MAG
24	111.5	80.2	373	3	Aab24242 Human Nogo

25	111.5	80.2	373	4	Aab82350 Human NOG
26	111.5	80.2	373	5	Aam47954 Human RTN
27	111.5	80.2	373	5	Abg30337 Human Nog
28	111.5	80.2	373	5	Abg68601 Human pan
29	111.5	80.2	373	5	Abg81079 Human neu
30	111.5	80.2	373	7	Adi63044 Human apo
31	111.5	80.2	373	7	Adi63044 Human RTN
32	111.5	80.2	373	8	Adp97235 Human NOG
33	111.5	80.2	960	9	Ady70654 Human BAC
34	111.5	80.2	973	8	Adq16420 Fusion pr
35	111.5	80.2	1178	3	Aay71311 Human neu
36	111.5	80.2	1192	3	Aay56967 Human MAG
37	111.5	80.2	1192	4	Abg82349 Human NOG
38	111.5	80.2	1192	4	Aau04591 Human NOG
39	111.5	80.2	1192	5	Abg30938 Human pan
40	111.5	80.2	1192	5	Abg68600 Human pan
41	111.5	80.2	1192	5	Abb81078 Human neu
42	111.5	80.2	1192	6	Abt59667 Human NOG
43	111.5	80.2	1192	7	Adk67502 Human RTN
44	111.5	80.2	1192	8	Ado08103 Human pol
45	111.5	80.2	1192	8	Ado26400 Human tru

ALIGNMENTS

RESULT 1

AAY71561
ID AAY71561 standard; protein; 171 AA.

AC AAY71561;

XX 02-NOV-2000 (first entry)

DT Rat Nogo A protein fragment used in the construction of mutant NiR.

DE Rat Nogo A protein fragment used in the construction of mutant NiR.

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;

KW central nervous system; neoplastic disease; antiproliferative; glioma;

KW antisense gene therapy; neuroblastoma; meningioma; ratioblastoma;

KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;

KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;

KW structural plasticity; screening; mutant; muten.

XX Rattus sp.

XX WO200031235-A2.

XX 02-JUN-2000.

XX 05-NOV-1999; 99WO-US026160.

XX 06-NOV-1998; 98US-0107446P.

XX (SCHW/) SCHWAB M E.

XX (CHEN/) CHEN M S.

XX Schwab ME, Chen MS;

XX WPI, 2000-400052/34.

XX Nogo proteins and nucleic acids useful for treating neoplastic disorders

XX of the central nervous system and inducing regeneration of neurons.

XX Example; Page; 122pp; English.

XX The patent relates to neurite growth inhibitor Nogo which is free of all

XX central nervous system (CNS) myelin material with which it is native

XX associated. Nogo proteins and fragments displaying neurite growth

XX inhibitory activity are used in the treatment of neoplastic disease of

XX the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,

XX ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,

XX oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and

degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of CNS neurons or to promote structural plasticity of CNS in disorders where axonal growth, regeneration or maintenance are deficient e.g. where axonal myelin, CNS disorders and/or trauma are the aetiological factors. The administration of disorders and to access for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is a fragment of rat Nogo-A protein shown in AAV7110, which is used in the construction of mutant N1R. The mutant is composed of His-tag/Tag/vector/Nogo-A sequence aa 1-171/vector. Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAV7110. SEQ ID numbers 35-42 are referred to in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers

sequence 171 AA:

	RESULT 2	
AA7Y1558	AA7Y1558 standard; protein; 359 AA.	
ID	AA7Y1558	
XX	AC	
XX	AA7Y1558;	
DT	02-NOV-2000	(first entry)
DE	Rat Nogo A protein fragment used in the construction of mutant Nogo-B.	
XX		
KW	Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;	
KW	central nervous system; neoplastic disease; antiproliferative; glioma;	
KW	antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;	
KW	degenerative nerve disease; Alzheimer's disease; Parkinson's disease;	
KW	hyperproliferative disorder; benign dysproliferative disorder; diagnosis;	
KW	psoriasis; tissue hypertrophy; neuronal regeneration; treatment;	
KW	structural plasticity; screening; mutant; mutein.	
OS	Rattus sp.	
XX		
Key	Location/Qualifiers	
FT	1..171	
Region	/note= "Corresponds to residues 1-171 of rat Nogo A protein shown in AA7Y1310"	
FT	172..359	
Region	/note= "Corresponds to residues 975-1162 of rat Nogo A protein shown in AA7Y1310"	
FT		
FT		
PN	WO2000031235-A2.	
XX		
PD	02-JUN-2000.	
PP	05-NOV-1999; 99WO-US026160.	
PR	06-NOV-1998; 98US-0107446P.	
PA	(SCHW/) SCHWAB M E.	
PA	(CHEN/) CHEN M S.	
XX		

PI Schwab ME, Chen MS;
 XX WPT: 2000-400052/34.
 XX
 XX
 XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
 XX of the central nervous system and inducing regeneration of neurons.
 XX
 XX Example; Page, 122pp; English.
 XX
 XX The patent relates to neurite growth inhibitor Nogo which is free of all
 XX central nervous system (CNS) myelin material with which it is natively
 XX associated. Nogo Proteins and fragments displaying neurite growth
 XX inhibitory activity are used in the treatment of neoplastic disease of
 XX the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
 XX ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
 XX oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and
 XX degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
 XX Therapeutics which promote Nogo activity can be used to treat or prevent
 XX hyperproliferative or benign dysproliferative disorders e.g. psoriasis
 XX and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
 XX used to inhibit production of Nogo protein to induce regeneration of
 XX neurons or to promote structural plasticity of the CNS in disorders where
 XX neurite growth, regeneration or maintenance are deficient or desired. The
 XX animal models can be used in diagnostic and screening methods for
 XX readiposition to disorders and to screen for or test molecules which can
 XX treat or prevent disorders or diseases of the CNS. The present sequence
 XX is derived by fusing two fragments of rat Nogo A protein shown in
 XX AA7V1310. The fragment is used in the construction of mutant Nogo-B. The
 XX mutant is composed of His-tag/T7-tag/vector/Nogo-A sequence aa 1-171 +
 XX 975-1162. Nogo A deletion mutants were used for mapping the inhibitory
 XX sites of Nogo protein. Major inhibitory region was identified in the Nogo
 XX A sequence from amino acids 172-974, particularly amino acids 542-722. In
 XX addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3
 XX fibroblast spreading. Note: The present sequence is not given in the
 XX specification but is derived from rat Nogo A sequence shown in AA7V1310.
 XX SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in
 XX disclosure of the specification. However, the specification does not
 XX include sequences for these SEQ ID numbers

CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjogren-Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (IgA- and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangiectasia, Friedreich's ataxia, amyloid polynuropathies,
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents the rat
CC neurotransmitter receptor protein Nogo-B, an example of NS-specific
CC antigen
XX
SQ Sequence 360 AA;

Query Match 100.0%; Score 139; DB 5; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDEDELEVL 27
Db 31 EPEDEDEDEDEDEDEDELEVL 57

RESULT 5
AAV71385
ID AAV71385 standard; protein; 361 AA.
AC AAV71385;
XX
DI 02-NOV-2000 (first entry)
DE
XX Alternative version of rat neurite growth inhibitor Nogo B.
XX
XX Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menigoma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening.
XX
OS Rattus sp.
XX
XX Location/Qualifiers
FH Key
FH Region
FT 1. .172
FT /note= "Corresponds to amino acids 1-172 of Nogo A
FT protein shown in AAV71310"
FT Inhibitory-site 1. .171
FT /note= "Inhibits NIH 3T3 fibroblast spreading"
FT Modified-site 30
FT /note= "Casein kinase II site"
FT Region 31. .58
FT /note= "Acidic region"
FT Region 173. .361
FT /note= "Corresponds to amino acids 975-1163 of Nogo A
FT protein (AAV71310)"
FT Region 174. .361
FT /note= "This region is common to Nogo A, B and C
FT isoforms"
FT Domain 186. .221
FT /label= Transmembrane domain
FT /note= "C-terminal hydrophobic region"
FT Modified-site 222
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 269. .271
FT /note= "Asn is N-glycosylated"
FT Modified-site 271
FT /note= "Protein kinase C (PKC) site"

FT Modified-site 287
FT /note= "Protein kinase C (PKC) site"
FT Domain 288. .323
FT /label= Transmembrane domain
FT /note= "C-terminal hydrophobic region"
FT Modified-site 339. .341
FT /note= "Asn is N-glycosylated"
FT Modified-site 341
FT /note= "Protein kinase C (PKC) site"
XX
XX WO200031235-A2.
XX
XX 02-JUN-2000.
XX
XX 05-NOV-1999; 99WO-US026160.
XX
XX 06-NOV-1998; 98US-0107446P.
XX
XX (SCHWAB) SCHWAB M E.
XX (CHEN) CHEN M S.
XX Schwab ME, Chen MS;
XX WPI; 2000-400052/34.
XX
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX of the central nervous system and inducing regeneration of neurons.
XX
XX Claim 4; Page; 122pp; English.
XX
XX The present sequence is an alternative version of rat Nogo B protein
XX which is a potent neural cell growth inhibitor and is free of all central
XX nervous system (CNS) myelin material with which it is native
XX associated. The Nogo B transcript arises as a result of alternative
XX splicing of Nogo gene. Nogo proteins and fragments displaying neurite
XX growth inhibitory activity are used in the treatment of neoplastic
XX disease of the CNS e.g. glioma, glioblastoma, medulloblastoma,
XX craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic
XX neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma
XX and degenerative nerve diseases e.g. Alzheimer's and Parkinson's
XX diseases. Therapeutics which promote Nogo activity can be used to treat
XX or prevent hyperproliferative or benign dysproliferative disorders e.g.
XX psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic
XX acids can be used to inhibit production of Nogo protein to induce
XX regeneration of neurons or to promote structural plasticity of the CNS in
XX disorders where neurite growth, regeneration or maintenance are deficient
XX or desired. The animal models can be used in diagnostic and screening
XX methods for predisposition to disorders and to screen for or test
XX molecules which can treat or prevent disorders or diseases of the CNS.
XX Note: The present sequence is not given in the specification but is
XX derived from Nogo A protein sequence (AAV71310) and corresponds to
XX residues 1-172 fused to 975-1163 of Nogo A. This sequence is an
XX alternative version of the Nogo B sequence (see AAV71383) described in
XX the specification as being residues 1-172 fused to C-terminal 188 amino
XX acids (residues 976-1163) of Nogo A. SEQ ID numbers 35-42 are referred in
XX claim 32 and SEQ ID NO: 29 in disclosure of the specification. However
XX the specification does not include sequences for these SEQ ID numbers
XX
XX Sequence 361 AA;

Query Match 100.0%; Score 139; DB 3; Length 361;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDELEVL 27
Db 31 EPEDEDEDEDEDEDELEVL 57

RESULT 6
ADE85283
ID ADE85283 standard; protein; 379 AA.
XX

AC ADB85283;
XX 04-DEC-2003 (first entry)
XX Rat fccen-m2 reticulon SEQ ID NO:164.
XX rat; streptozocin; kinase; phosphatase; ion channel protein; receptor;
KW transporter; G-protein coupled receptor; GPCR; DNA-binding proteins;
KW protease; enzyme; analgesic; gene therapy; pain; diabetes.
XX
XX Rattus norvegicus.
XX
XX EPI284297-A2.
XX 19-FEB-2003.
XX 26-JUL-2002; 2002EP-00255228.
XX 27-JUL-2001; 2001GB-00018354.
PR 07-FEB-2002; 2002GB-00002880.
XX
XX (WARN) WARNER LAMBERT CO.
XX
XX Brookbank RA, Dixon AK, Lee K, Pincock RD;
XX WPI; 2003-364994/35.
XX N-PSDB; ADB85284.
XX
XX Use of gene sequence that is down-regulated in response to streptozocin-
PT induced diabetes, vector, host cell, animal, polypeptide and antibody, in
PT screening of compounds for treating or diagnosing pain.
XX
XX Disclosure; Page 239-240; 256pp; English.
XX
XX The invention relates to a novel isolated gene sequence that is down-
CC regulated in the spinal cord in response to streptozocin-induced
CC diabetes, or comprising, hybridizing or having at least 80% sequence
CC identity to a sequence whose expression products are kinases,
CC phosphatases, ion channel proteins, receptors, transporters, G-protein
CC coupled receptor proteins, DNA-binding proteins, proteases or enzymes,
CC given in the specification. A gene of the invention has analgesic
CC activity, and may have a use in gene therapy. The gene sequences, vector,
CC host cell, animal, polypeptide and antibody are useful for screening of
CC compounds for diagnosing or treating pain. The kits are useful for
CC simultaneous separate or sequential detecting and/or quantifying down-
CC regulation of a gene sequence in the spinal cord of a mammal in response
CC to streptozocin-induced diabetes. The compound or pharmaceutical
CC composition is useful as a medicament for treating or diagnosing pain.
CC The present sequence represents a protein encoded by a gene of the
CC invention.
XX
XX Sequence 379 AA;
SQ

Query Match 100.0%; Score 139; DB 7; Length 379;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDEDEDEDELEVL 27
DB 31 EPEDEDEDEDEDEDEDEDEDEDELEVL 57

RESULT 7
AAV71560
ID AAV71560 standard; protein; 974 AA.
XX
XX AAV71560;
XX
XX 02-NOV-2000 (first entry)
XX
XX Rat Nogo A protein fragment used in the construction of mutant NiAext.
DE
XX Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW

KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; mutant; mitein.
XX
XX Rattus sp.
OS
XX
XX WO2000031235-A2.
PN
XX
XX 02-JUN-2000.
PD
XX
XX 05-NOV-1999; 99WO-US026160.
XX
XX 06-NOV-1998; 98US-0107446P.
PR
XX
XX (SCHW/) SCHWAB M R.
XX (CHEN/) CHEN M S.
PA
XX
XX Schwab ME, Chen MS;
PI
XX
XX WPI; 2000-400052/34.
DR
XX
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX of the central nervous system and inducing regeneration of neurons.
XX
XX Example; Page; 122pp; English.
XX
XX The patent relates to neurite growth inhibitor Nogo which is free of all
CC central nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic disease of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyma, pinealoma, haemangioblastoma, acoustic neuroma
CC oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The
CC animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which can
CC treat or prevent disorders or diseases of the CNS. The present sequence
CC is a fragment of rat Nogo A protein shown in AAV71310, which is used in
CC the construction of mutant NiAext. The mutant is composed of His-tag/T7-
CC tag/vector/Nogo-A sequence aa 1-974/T7-tag. Nogo A deletion mutants were
CC used for mapping the inhibitory sites of Nogo protein. Major inhibitory
CC region was identified in the Nogo A sequence from amino acids 172-974,
CC particularly amino acids 542-722. In addition, N-terminal region 1-171
CC was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
CC present sequence is not given in the specification but is derived from
CC rat Nogo A sequence shown in AAV71310. SEQ ID numbers 35-42 are referred
CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC However, the specification does not include sequences for these SEQ ID
CC numbers
XX
XX Sequence 974 AA;
SQ

Query Match 100.0%; Score 139; DB 3; Length 974;
Best Local Similarity 100.0%; Pred. No. 8.1e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDEDEDEDELEVL 27
DB 31 EPEDEDEDEDEDEDEDEDEDEDELEVL 57

RESULT 8
AAV71557
ID AAV71557 standard; protein; 1162 AA.

[illegible]

FT /note= "Protein kinase C (PKC) site"
FT 850
FT /note= "Protein kinase C (PKC) site"
FT 855
FT /note= "Protein kinase C (PKC) site"
FT 863
FT /note= "Casein kinase II site"
FT 868
FT /note= "Protein kinase C (PKC) site"
FT 893
FT /note= "Protein kinase C (PKC) site"
FT 912. .914
FT /note= "Asn is N-glycosylated"
FT 925. .927
FT /note= "Asn is N-glycosylated"
FT 954
FT /note= "PKC and casein kinase II sites"
FT 956
FT /note= "PKC and casein kinase II sites"
FT 975. 1162
FT /note= "This region is not essential for inhibitory
FT activity."
FT 976. 1163
FT /note= "C-terminal common region found in Nogo A, B and C
FT isoforms"
FT 988. 1023
FT /label= Transmembrane domain
FT /note= "C-terminal hydrophobic region specifically
FT described in claim 16"
FT 1024
FT /note= "Protein kinase C (PKC) site"
FT 1071. 1073
FT /note= "Asn is N-glycosylated"
FT 1073
FT /note= "Protein kinase C (PKC) site"
FT 1089
FT /note= "Protein kinase C (PKC) site"
FT 1090. 1125
FT /label= Transmembrane domain
FT /note= "C-terminal hydrophobic region specifically
FT described in claim 16"
FT 1141. 1143
FT /note= "Asn is N-glycosylated"
FT 1143
FT /note= "Protein kinase C (PKC) site"
FT
XX WO200031235-A2.
XX
XX
XX 02-JUN-2000.
XX
XX 05-NOV-1999; 99WO-US026160.
XX
XX 06-NOV-1998; 98US-0107446P.
XX (SCHW/) SCHWAB M E.
XX (CHEN/) CHEN M S.
XX
XX Schwab ME, Chen MS;
XX
XX WPI; 2000-400052/34.
XX N-PSDB; AAD01173.
XX
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX of the central nervous system and inducing regeneration of neurons.
XX
XX Claim 3; Fig 2A; 122pp; English.
XX
XX The present sequence is a rat Nogo A protein which is a potent neural
XX cell growth inhibitor and is free of all central nervous system (CNS)
XX myelin material with which it is natively associated. The protein was
XX derived from a cDNA generated by fusing R018U37-3, R1-3U21 cDNAs isolated
XX from hexanucleotide-primed rat brain stem/spinal cord library, and Oll18
XX cDNA from an oligo d(T)-primed rat oligodendrocyte library. Nogo proteins

CC and fragments displaying neurite growth inhibitory activity are used in
CC the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
CC haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma,
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
CC activity can be used to treat or prevent hyperproliferative or benign
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
CC Ribosomes or antisense Nogo nucleic acids can be used to inhibit
CC production of Nogo protein to induce regeneration of neurons or to
CC promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: The present sequence
CC designated as SEQ ID NO: 2 is stated to be the same as the sequence shown
CC in Fig. 13 (see AAY71384) of the specification. However, this sequence
CC does not match the sequence given in Fig. 13. SEQ ID numbers 35-42 are
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However, the specification does not include sequences for
CC these SEQ ID numbers
XX
XX Sequence 1163 AA;
SQ
Query Match 100.0%; Score 139; DB 3; Length 1163;
Best Local Similarity 100.0%; Pred. No. 9.7e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPEDEDEDEDEDEDEDEDEDEDELEVL 27
DB 31 EPEDEDEDEDEDEDEDEDEDEDELEVL 57
RESULT 10
AAY71384
ID AAY71384 standard; protein; 1163 AA.
XX
XX AC AAY71384;
XX
XX 02-NOV-2000 (first entry)
XX
XX Alternative version of rat neurite growth inhibitor Nogo A.
XX
XX Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
XX central nervous system; neoplastic disease; antiproliferative; glioma;
XX antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
XX degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
XX hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
XX psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
XX structural plasticity; screening.
XX
XX Rattus sp.
XX
XX OS
XX
XX Key Location/Qualifiers
XX Inhibitory-site 1. .171
XX /note= "Inhibits NIH 3T3 fibroblast spreading"
XX Modified-site 30
XX /note= "Casein kinase II site"
XX Region 31. .58
XX /note= "Acidic region"
XX Region 172. .259
XX /note= "This region is not essential for inhibitory
XX activity"
XX Misc-difference 223
XX /label= Unknown
XX /note= "There is Leu at this position in the sequence
XX shown in AAY71310"
XX
XX Modified-site 233
XX /note= "Protein kinase C (PKC) site"
XX Modified-site 242. .244
XX /note= "Asn is N-glycosylated"
XX Modified-site 291
XX /note= "Protein kinase C (PKC) site"

XX DE Rat neurotransmitter receptor protein Nogo-A.

XX KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;

XX KW central nervous system; peripheral nervous system; tranquilizer; Nogo;

XX KW vulnary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;

XX KW neurotrophic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;

XX KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;

XX KW neurotransmitter receptor; rat; receptor.

XX OS Rattus norvegicus.

XX US2002072493-A1.

XX PN 13-JUN-2002.

XX PD 28-JUN-2001; 2001US-00893348.

XX PF 19-MAY-1998; 98IL-00124500.

XX PR 21-JUL-1998; 98NO-US014715.

XX PR 22-DEC-1998; 98US-00218277.

XX PR 19-MAY-1999; 99US-00314161.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;

XX PI Moalem G;

XX DR N-PSDB; ABN86600.

XX WPI; 2002-607255/65.

XX DR N-PSDB; ABN86600.

XX Promoting nerve regeneration and preventing neuronal degeneration in the

XX PT central/peripheral nervous system from injury/disease, comprises

XX PT administering nervous system-specific activated T cells/antigen, or

XX PT analogs/peptides.

XX Example 5; Page 44-47; 93pp; English.

XX The invention relates to promoting nerve regeneration or conferring

XX neuroprotection and preventing or inhibiting neuronal degeneration in the

XX central/peripheral nervous system (NS). The method involves administering

XX NS-specific activated T cells, NS-specific antigen, its analogue or its

XX peptide, a nucleotide sequence the NS-specific antigen or its analogue or

XX combinations. The method is useful for promoting nerve regeneration and

XX preventing neuronal degeneration in central/peripheral nervous system

XX from injury/disease, where the injury is spinal cord injury, blunt

XX trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or

XX damages caused by surgery such as tumour excision. The disease is not an

XX autoimmune disease or neoplasm. The disease results in a degenerative

XX process occurring in either gray or white matter or both. The disease is

XX diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's

XX disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,

XX amyotrophic lateral sclerosis, non-artritic optic neuropathy, and

XX vitamin deficiency, intervertebral disc herniation, prion diseases such

XX as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral

XX neuropathies associated with various diseases, including but not limited

XX to uremia, porphyria, chronic ataxic neuropathy, biliary cirrhosis, primary

XX sensory neuropathy, hypoglycemia, Sjogren-Larsson syndrome, acute

XX amyloidosis, obstructive lung diseases, acromegaly, malabsorption

XX syndromes, polycythemia vera, immunoglobulin (IgA- and IgG gamma-

XX pathies, complications of various drugs (e.g., metronidazole) and toxins

XX (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia

XX telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,

XX adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's

XX disease, or lipoproteinemia. The present sequence represents the rat

XX neurotransmitter receptor protein Nogo-A, an example of NS-specific

XX antigen

XX Sequence 1163 AA;

XX Query Match 100.0%; Score 139; DB 5; Length 1163;

XX Best Local Similarity 100.0%; Pred. No. 9.7e-07;

XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPDEDEDEDEDEDEDEDEDEDELEVL 27

Db 31 EPDEDEDEDEDEDEDEDEDEDELEVL 57

RESULT 12

ADO26399

ID ADO26399 standard; protein; 1163 AA.

XX ADO26399;

XX 29-JUL-2004 (first entry)

XX Rat truncated Nogo-A protein.

XX rat; human; Nogo-A; truncated; affinity; membrane-bound protein.

XX Rattus sp.

XX WO2004039836-A1.

XX 13-MAY-2004.

XX 31-OCT-2002; 2002WO-EP012210.

XX 31-OCT-2002; 2002WO-EP012210.

XX (PIER-) PIERIS PROTEOLAB AG.

XX Skerra A, Fiedler M;

XX WPI; 2004-376159/35.

XX New isolated truncated Nogo-A polypeptide that corresponds to a truncated

XX form of the Nogo-A protein, useful for identifying a compound having

XX detectable affinity to a Nogo-A protein.

XX Claim 1; Fig 6A; 80pp; English.

XX The present invention relates to an isolated truncated Nogo-A polypeptide

XX that corresponds to a truncated form of the Nogo-A protein from the rat

XX and from the human. The truncated polypeptide is useful for identifying a

XX compound having detectable affinity to a Nogo-A protein. The present

XX sequence is a Nogo-A polypeptide of the invention.

XX Sequence 1163 AA;

XX Query Match 100.0%; Score 139; DB 8; Length 1163;

XX Best Local Similarity 100.0%; Pred. No. 9.7e-07;

XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPDEDEDEDEDEDEDEDEDEDELEVL 27

Db 31 EPDEDEDEDEDEDEDEDEDEDELEVL 57

RESULT 13

ADP45572

ID ADP45572 standard; protein; 1163 AA.

XX ADP45572;

XX 09-SEP-2004 (first entry)

XX Rat NogoA protein SEQ ID NO:26.

XX binding molecule; human; NogoA; NiG-D20; NogoA_623-640;

XX nerve repair; neuroprotective; gene therapy;

XX central nervous system injury; CNS injury; neurodegenerative disorder;

XX Rattus norvegicus.

XX OS

XX Mus musculus Nogo protein.
DE
XX Nerve regeneration; gene therapy; vaccine; neuroprotective; nootropic;
KW Nogo; mouse.
XX
XX Mus musculus.
OS
XX US2004191240-A1.
PN
XX 30-SEP-2004.
PD
XX 31-JUL-2003; 2003US-00633423.
PF
XX 28-MAR-2003; 2003JP-00092923.
PR
XX 30-APR-2003; 2003US-00427741.
PX
XX (TOHY/) TOHYAMA M.
PA (YANA/) YAMASHITA T.
XX
XX Tohyama M, Yamashita T;
PI
XX WPI, 2004-698659/68.
DR N-PSDB; ADR89536.
DR
XX Regenerating nerves or modulating nerve regeneration comprises inhibiting
PT or modulating p75 signal transduction pathway by administering a
PT transduction agent, e.g. p21 or Rho, or an agent that interacts with the
PT transduction agent.
PT
XX
XX Example 2; SEQ ID NO 10; 209pp; English.
PS
XX The present invention relates to a method for regenerating nerves or
CC modulating nerve regeneration. The method involves inhibiting or
CC modulating a p75 signal transduction pathway. The invention is useful for
CC treating, preventing or diagnosing neurological diseases based on nerve
CC regeneration and for identifying agents useful for nerve regeneration.
CC The invention is also useful in gene therapy and for preparing vaccine.
CC The present sequence is the Mus musculus Nogo protein. Note: This
CC sequence is said to encoded by SEQ ID NO 9, however this does not appear
CC to be the same.
XX
XX Sequence 1162 AA;
SQ
Query Match 86.0%; Score 119.5; DB 8; Length 1162;
Best Local Similarity 92.6%; Pred. No. 0.00012;
Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 EFDEDEDEDEDEDEDEDELEVL 27
DB 31 EFDEDEDEDEDEDEDEDELEVL 56
Search completed: February 17, 2006, 03:49:29
Job time : 127.333 secs

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OM protein - protein search, using sw model

Run on: February 17, 2006, 03:49:55 ; Search time 19.3333 Seconds
(without alignments)
134.372 Million cell updates/sec

Title: US-09-830-972A-2_COPY_31_57
Perfect score: 139
Sequence: 1 EPEDEDEDEDEDEDEDELEVL 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match %	Length	DB	ID	Description
1	97	69.8	186	2	S30221	nonhistone chromos
2	97	69.8	209	1	NSHUH2	nonhistone chromos
3	97	69.8	792	2	T42963	hypothetical prote
4	95	68.3	210	2	S54774	high mobility grou
5	94	67.6	1300	2	T03166	probable immediate
6	93	66.9	896	2	T24169	hypothetical prote
7	93	66.9	906	2	T24166	hypothetical prote
8	92	66.2	376	2	T10455	heat shock related
9	90.5	65.1	210	2	A34719	nonhistone chromos
10	90	64.7	387	2	S02708	troponin T - fruit
11	90	64.7	396	2	S13251	troponin T - fruit
12	90	64.7	5037	2	S15041	ryanodine receptor
13	89	64.0	589	2	T52070	RNAL protein homol
14	89	64.0	589	2	A36983	RNAL homolog flgi
15	88.5	63.7	406	2	A48059	oncoprotein zc-Myc
16	88	63.3	201	2	A88363	protein f26h11.1
17	88	63.3	244	2	T21434	hypothetical prote
18	88	63.3	412	2	A55320	immunophilin FKBP4
19	88	63.3	420	2	B86217	protein T27G7.4
20	88	63.3	678	2	A54514	glutamic acid-rich
21	88	63.3	694	1	DNCHNL	nucleolin - chicke
22	88	63.3	1078	2	T42712	myelin transcripti
23	88	63.3	5035	1	I46646	ryanodine receptor
24	87	62.6	207	2	JC1129	nonhistone chromos
25	87	62.6	207	2	JC1114	high-mobility grou
26	87	62.6	210	2	S62355	high-mobility grou
27	87	62.6	215	2	S02826	nonhistone chromos
28	87	62.6	216	2	S29857	nonhistone chromos
29	87	62.6	325	2	T18283	hypothetical prote

RESULTS

S30221
nonhistone chromosomal protein HMG-2B - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S30221
R:Alexandre, S.; Li, W. W.; Lee, A. S.
Nucleic Acids Res. 20, 6413, 1992
A:Title: A human HMG2 cDNA with a novel 3'-untranslated region.
A:Reference number: S30221; MUID:93117123; PMID:1475204
A:Accession: S30221
A>Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: RNA
A:Residues: 1-186 <NLE>
A:Cross-references: UNIPROT:P26583; UNIPARC:UPI000016AA6C; EMBL:Z17240; NID:g32334; PIDN:
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992
C:Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C:Keywords: chromosomal protein (fragment) <HMG>
F:1-60/Domain: HMG box homology (fragment) <HMG>
F:69-143/Domain: HMG box homology <HMG1>

Query Match 69.8%; Score 97; DB 2; Length 186;
Best Local Similarity 73.9%; Pred. NO. 0.022; 1; Indels 0; Gaps 0;
Matches 17; Conservative 5; Mismatches 1

QY 1 EPEDEDEDEDEDEDEDELEEE 23
| | | | | : | | | | | : | | : | |
DB 163 EPEDEDEDEDEDEDEDEDEDE 185

RESULTS

NSHUH2
nonhistone chromosomal protein HMG-2 - human
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: A42425; S20061; S18068
R:Shirakawa, H.; Yoshida, M.
J. Biol. Chem. 267, 6641-6645, 1992
A:Title: Structure of a gene coding for human HMG2 protein.
A:Reference number: A42425; MUID:92202209; PMID:1551873
A:Accession: A42425
A:Molecule type: DNA
A:Residues: 1-2509 <SHI>
A:Cross-references: UNIPROT:P26583; UNIPARC:UPI000012CA25; GB:M83665; NID:g184235; PIDN:
A>Note: sequence extracted from NCHI backbone (NCBIN:89899, NCBI:P:89900)
R:Note: Initiator Met not shown
R:MaJumdar, A.; Brown, D. Kerby, S.; Rudzinski, I.; Polte, T.; Randhawa, Z.; Seidman, M
Nucleic Acids Res. 19, 6643-1961
A:Title: Sequence of human HMG2 cDNA.
A:Reference number: S20061; MUID:92093633; PMID:1754403
A:Accession: S20061
A:Molecule type: mRNA


```

A:Gene: CESP.RIIA5.la
A:Map position: 1
A:A:introns: 14/2; 40/3; 277/3; 318/3; 363/3; 560/1; 668/1; 808/3

Query Match      66.9%; Score 93; DB 2; Length 906;
Best Local Similarity 68.0%; Pred. No. 0.22;
Matches 17; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 EPDEDEDEDEDEDEDELE 25
   |.:|.|.|.|.|.|.|.|.|.:|
DB 586 EDDDDDEDEDEDEDEDEE 610

Tt10455
heat shock related protein - Plasmodium berghei
C:Species: Plasmodium berghei
C:CDate: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: Tt10455
Mol. Biochem. Parasitol. 83, 25-33, 1996
A:A>Title: Further characterization of a 58 kDa Plasmodium berghei phosphoprotein as a codon optimized gene
A:Reference number: Z17026; MUID: 97164116; PMID: 9010839
A:Accession: Tt10455
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-376 <WIS>
A:Cross-references: UNIPROT:O08168; UNIPARC:UPI000016BP72; EMBL:L04508; NID:g309691; PIR:S02708
A:Experimental source: strain ANKA
A:Keywords: molecular chaperone

Query Match      66.2%; Score 92; DB 2; Length 376;
Best Local Similarity 59.3%; Pred. No. 0.12;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 EPDEDEDEDEDEDEDELEVL 27
   |.:|.|.|.|.|.|.|.|.:|
DB 14 EKSDDEDEDEDEDEDDPEKLELI 40

RESULT 9
A34719
nonhistone chromosomal protein HMG-2 - pig
C:Species: Sus scrofa domestica (domestic pig)
C:CDate: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
C:Accession: A34719
R.Shirakawa, H.; Teuda, K.; Yoshida, M.
Biochemistry 29, 4419-4423, 1990
A:A>Title: Primary structure of non-histone chromosomal protein HMG2 revealed by the nucleotide sequence
A:Reference number: A34719; MUID: 90275208; PMID: 2350545
A:Accession: A34719
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-210 <SHI>
A:Cross-references: UNIPROT:P17741; UNIPARC:UPI00016CC65; GB:J02895; NID:g164491; PIR:S02708
C:Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C:Keywords: chromosomal protein; DNA binding; nucleus
F:6-83/Domain: HMG box homology <HMG>
F:92-166/Domain: HMG box homology <HMG2>

Query Match      65.1%; Score 90.5; DB 2; Length 210;
Best Local Similarity 76.0%; Pred. No. 0.093;
Matches 19; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 1 EPDEDEDEEE--EDEDEDEDLE 22
   |.:|.|.|.|.|.|.|.|.:|
DB 186 EPDEDEDEDEDEDEDEDEE 210

RESULT 10
S02708
tropoinin T - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster

```

C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 16-Feb-1997

C:Accession: S02708
R:Flyberg, E.
J. Mol. Biol. 204, 621-637, 1988

A>Title: Troponin of asynchronous flight muscle.

A:Reference number: S02708; MUID:89141761; PMID:2852258

A:Accession: S02708

A:A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-387 <BUL>

A:Cross-references: UNIPARC:UPI000017BEE2

C:Genetics:

A:Gene: FlyBase: up

A:Cross-references: FlyBase:FBgn0004169

C:Keywords: muscle

Query Match 64.7%; Score 90; DB 2; Length 387;
Best Local Similarity 68.0%; Pred. No. 0.18;
Matches 17; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 EPEDDEDEDEDEDDLELE 25
|||||:||||:|:|
DB 348 EEDEDEDEDEDEDEDEE 372

RESULT 11

S13251
troponin T - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

A:Accession: S13251; S29482

R:Flyberg, E.; Flyberg, C.C.; Beall, C.; Saville, D.L.

J. Mol. Biol. 216, 657-675, 1990

A>Title: *Drosophila melanogaster* troponin-T mutations engender three distinct syndromes

A:Reference number: S13251; MUID:91080155; PMID:2124273

A:Accession: S13251

A:Molecule type: mRNA

A:Residues: 1-396 <FYRI>

A:Cross-references: UNIPROT:P19351; UNIPARC:UPI000017BEE3; EMBL:X54504

R:Flyberg, E.A.

submitted to the EMBL Data Library, August 1990

A:Reference number: S29482

A:Accession: S29482

A:Molecule type: mRNA

A:Residues: 1-191, 'A', 193-396 <FYR2>

A:Cross-references: UNIPARC:UPI0000137662; EMBL:X54504; NID:g8739; PID:g8740

C:Genetics:

A:Gene: FlyBase: up

A:Cross-references: FlyBase:FBgn0004169

A:Map position: X

Query Match 64.7%; Score 90; DB 2; Length 396;
Best Local Similarity 68.0%; Pred. No. 0.19;
Matches 17; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 EPEDDEDEDEDEDDLELE 25
|||||:||||:|:|
DB 357 EEDEDEDEDEDEDEDEE 381

RESULT 12

B35041
ryanodine receptor, skeletal muscle - rabbit

N:Alternate names: calcium-release channel protein; junctional channel complex

C:Species: *Oryctolagus cuniculus* (domestic rabbit)

C>Date: 27-Jul-1990 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004

A:Accession: S04654; B35041; A36181; S33794; S32504

R:Takeshima, H.; Nishimura, S.; Watanabe, T.; Ishida, H.; Kangawa, K.; Minamino, N.; Matsumoto, Y.; Nakamura, R.

Nature 339, 439-445, 1989

A>Title: Primary structure and expression from complementary DNA of skeletal muscle ryanodine receptor

A:Reference number: S04654; MUID:89262082; PMID:2725677

A:Accession: S04654

A:Molecule type: mRNA

us-09-830-972a-2_copy_31_57.rpr

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```
Matches 17; Conservative 8; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      1 EPEDEDEDEDEDEDEDEDELEVL 27
        | :|:|||||:||||:|::|:
DB     208 EDEDEDEDEDEDEDEDEE-EEIDV 233
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Search completed: February 17, 2006, 03:56:51
Job time : 21.3333 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: February 17, 2006, 03:43:13 ; Search time 123.333 Seconds
(without alignments)
154.453 Million cell updates/sec
Title: US-09-830-972A-2_COPY_31_57
Perfect score: 139
Sequence: 1 BPEDEDEDEDEDEDEDELELEVL 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
Result No.	Score	Query Match	Length DB ID		
1	139	100.0	360	2	Q6IRL3 RAT
2	139	100.0	379	2	Q540J3 RAT
3	139	100.0	478	2	Q5UI23 RAT
4	139	100.0	1163	1	RTN4 RAT
5	119.5	86.0	356	2	Q8BH78 MOUSE
6	119.5	86.0	375	2	Q8K3G7 MOUSE
7	119.5	86.0	375	2	Q8BHF5 MOUSE
8	119.5	86.0	720	2	Q7TNB7 MOUSE
9	119.5	86.0	1162	2	Q8BGM9 MOUSE
10	119.5	86.0	1163	2	Q8K3G8 MOUSE
11	119.5	86.0	1245	2	Q5DIR9 MOUSE
12	111.5	80.2	185	2	Q53R94 HUMAN
13	111.5	80.2	373	2	Q7L7Q6 HUMAN
14	111.5	80.2	392	2	Q96B16 HUMAN
15	111.5	80.2	1192	1	RTN4 HUMAN
16	111.5	80.2	1192	2	Q7L7Q8 HUMAN
17	100	71.9	343	2	Q6IPN0 HUMAN
18	99.5	71.6	306	2	Q6Z867 ORYZA
19	97	69.8	208	1	RMG2 HUMAN
20	97	69.8	209	2	Q5U072 HUMAN
21	97	69.8	496	2	Q6Q138 RAT
22	97	69.8	792	2	Q9YTL7 HERP
23	96	69.1	222	2	Q6PUE4 BRABE
24	96	69.1	456	2	Q5GF04 BRARE
25	96	69.1	496	2	Q5R1Z4 BRARE
26	96	69.1	639	2	Q8I1Y6 PLAF7
27	96	69.1	2649	1	Q7RAS7 PLAYO
28	95	68.3	209	1	RMG2 MOUSE
29	95	68.3	746	2	Q54VB9 DICDI
30	95	68.3	1205	2	Q54J58 DICDI
31	94	67.6	227	1	CHIC1_MOUSE

32	94	67.6	374	2	Q94K07 ARATH
33	94	67.6	374	2	Q9LTS5 ARATH
34	94	67.6	407	2	Q9TX81 PLASMODIUM
35	94	67.6	665	2	Q6L796 IPOPO
36	94	67.6	683	2	Q6INQ5 XENOPUS LAE
37	94	67.6	1274	2	Q5C054 CRYPV
38	94	67.6	1300	2	Q36421 GAGWA
39	94	67.6	1428	2	Q4YU61 PLABE
40	94	67.6	1472	2	Q54KK9 DICDI
41	94	67.6	1716	2	Q7M732 MOUSE
42	93	66.9	216	2	Q90228 AMBOSTOMA M
43	93	66.9	235	2	Q51D17 ENTHI
44	93	66.9	300	2	Q4SCS8 TETNG
45	93	66.9	391	2	Q4XW2 PLACH

ALIGNMENTS

RESULT 1
Q6IRL3 RAT PRELIMINARY; PRT; 360 AA.
AC Q6IRL3; DT 05-JUL-2004 (TREMREL. 27, Created)
DT 05-JUL-2004 (TREMREL. 27, Last sequence update)
DT 13-SEP-2005 (TREMREL. 31, Last annotation update)
DE RTN4 protein (RTN4-B1).
GN Name=RTN4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung and Placenta;
RX MEDLINE=2438257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haigh E.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Villalon D.K., Muzny D.M., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX Submitted (MAY-2004) to the ENBL/GenBank/DBJ databases.
RA Strausberg R.;
RN (3)
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22715987; PubMed=12832288;
RA Certle T., Klingner M., Stuermer C.A., Schwab M.E.;
RT "A reticular rapoddy: phylogenetic evolution and nomenclature of the
RT RTN/Nogo gene family".
RN FASEB J. 17:1238-1247(2003).
RN (4)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RG NIH MGC Project;

Tue Feb 21 15:13:29 2006

Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RA EMBL: BC070879; AAH70879.1; -; mRNA.
 RA EMBL: AY164740; AAH74740.1; -; mRNA.
 RA EMBL: BC097936; AAH97936.1; -; mRNA.
 RA GO: GO:0005783; C:cytoplasmic reticulum; IEA.
 RA InterPro: IPR003388; Reticulon.
 RA Pfam: PF02453; Reticulon; 1.
 RA PROSITE: PS00845; RETICULON; 1.
 SQ SEQUENCE 360 AA; 38822 MW; 149714AD6C3D65A7 CRC64;

Query Match 100.0%; Score 139; DB 2; Length 360;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDEDEDEDEDEDEDEDEDELELEVL 27
 DB 31 EPDEDEDEDEDEDEDEDEDELELEVL 57

RESULT 2
 Q540J3 RAT PRELIMINARY; PRT; 379 AA.

AC Q540J3 RAT PRELIMINARY; PRT; 379 AA.
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE RTN4-B2;
 GN Name=Rtn4;

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22715887; PubMed=12832288;
 RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
 RT "A reticular rapscody: phylogenetic evolution and nomenclature of the
 RT RTN/Nogo gene family.";
 RL FASEB J. 17:1238-1247(2003).
 DR EMBL: AY164741; AAP47316.1; -; mRNA.
 SQ SEQUENCE 379 AA; 40719 MW; 9F15AB942D36ED0F CRC64;

Query Match 100.0%; Score 139; DB 2; Length 379;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDEDEDEDEDEDEDEDEDELELEVL 27
 DB 31 EPDEDEDEDEDEDEDEDEDELELEVL 57

RESULT 3

Q5UI23 RAT PRELIMINARY; PRT; 478 AA.

AC Q5UI23 RAT PRELIMINARY; PRT; 478 AA.
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Rtn4 protein (Fragment).
 GN Name=Rtn4;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards D., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smal M.A.,
 RA Scherf A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Heart;
 RG NIH MOC Project;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC086375; AAH86375.1; -; mRNA.

FT NON_TER 478 478
 SQ SEQUENCE 478 AA; 51326 MW; B5A1E421A3541D2A CRC64;

Query Match 100.0%; Score 139; DB 2; Length 478;

Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDEDEDEDEDEDEDEDEDELELEVL 27
 DB 31 EPDEDEDEDEDEDEDEDEDELELEVL 57

RESULT 4

RTN4 RAT STANDARD; PRT; 1163 AA.

AC Q9JX11; Q9JX10; Q9R009; Q9WU93; Q9WU00;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foccen)
 DE (Glut4 vesicle 20 kDa protein).
 GN Name=Rtn4; Synonym=Nogo;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]

RP NUCLEOTIDE SEQUENCE (ISOFORM 3), AND PARTIAL PROTEIN SEQUENCE.

RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;
 EX MEDLINE=99249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6;
 RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;
 RT "Cloning and characterization of a 22 kDa protein from rat adipocytes:
 RT a new member of the reticulon family.";
 RL Biochim. Biophys. Acta 1450:68-76(1999).
 RN [2]

RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).

EX MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219;
 RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
 RA Spillmann A., Christ F., Schwab M.E.;
 RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
 RT antigen for monoclonal antibody IN-1.";
 RL Nature 403:434-439(2000).
 RN [3]

RP NUCLEOTIDE SEQUENCE (ISOFORMS 2 AND 4).

RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;
 RA Ito T., Schatz S.M.;
 RT Cloning of a member of the reticulon gene family in rat: one of two
 RT minor splice variants";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

Db 31 EPEDEDEDEE-EEDEDEDELEVL 56

RESULT 6

Q8K3G7_MOUSE

AC Q8K3G7_MOUSE PRELIMINARY; PRT; 357 AA.

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Nogo-B.

GN Name=Rtn4;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

UN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=BALB/c;

RA Jin W., Li R., Long M., Shen J., Ju G.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY114153; AAM77069.1; -; mRNA.

DR MGI; MGI:1915835; Rtn4.

DR GO; GO:0042995; C:cell projection; IDA.

DR GO; GO:0043025; C:cell soma; IDA.

DR GO; GO:0005783; C:endoplasmic reticulum; IDA.

DR GO; GO:0005151; P:protein binding; IPI.

DR GO; GO:0001525; P:angiogenesis; IMP.

DR GO; GO:0007399; P:neurogenesis; IDA.

DR InterPro: IPR003388; Reticulon.

DR Pfam: PF02453; Reticulon; 1.

DR PROSITE: PS50845; RETICULON; 1.

SQ SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;

Query Match 86.0%; Score 119.5; DB 2; Length 357;

Best Local Similarity 92.6%; Pred. No. 0.0082;

Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPEDEDEDEE-EEDEDEDELEVL 27

DB 31 EPEDEDEDEE-EEDEDEDELEVL 56

RESULT 7

Q8BHF5_MOUSE

AC Q8BHF5_MOUSE PRELIMINARY; PRT; 375 AA.

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Rtn4 (Reticulon 4).

GN Name=Rtn4; ORFNames=RP23-17605.4-006;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

UN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=129/SvcJ7; and 129/SvcJ7;

RC MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;

RA Oertle T., Huber C., van der Putten H., Schwab M.E.;

RT "Genomic structure and functional characterisation of the promoters of

RT human and mouse nogo/rtn4.";

RL J. Mol. Biol. 325:299-323(2003).

UN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=129/SvcJ7;

RC Van der Putten H.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

RP [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=129/SvcJ7;

RA Van der Putten H., Mir A.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

RN [4]

RP NUCLEOTIDE SEQUENCE.

RA Kay M.;

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY102282; AAM73504.1; -; mRNA.

DR EMBL; AY102286; AAM73509.1; -; Genomic DNA.

DR EMBL; AL929371; CA124271.1; -; Genomic DNA.

DR Ensembl; ENSMUSG0000020458; Mus musculus.

DR MGI; MGI:1915835; Rtn4.

DR GO; GO:0042995; C:cell projection; IDA.

DR GO; GO:0043025; C:cell soma; IDA.

DR GO; GO:0005783; C:endoplasmic reticulum; IDA.

DR GO; GO:0005151; P:protein binding; IPI.

DR GO; GO:0001525; P:angiogenesis; IMP.

DR GO; GO:0007399; P:neurogenesis; IDA.

DR InterPro: IPR003388; Reticulon.

DR Pfam: PF02453; Reticulon; 1.

DR PROSITE: PS50845; RETICULON; 1.

SQ SEQUENCE 375 AA; 40300 MW; 23D9EB19BE671AE6 CRC64;

Query Match 86.0%; Score 119.5; DB 2; Length 375;

Best Local Similarity 92.6%; Pred. No. 0.0086; 0; Indels 1; Gaps 1;

Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPEDEDEDEE-EEDEDEDELEVL 27

DB 31 EPEDEDEDEE-EEDEDEDELEVL 56

RESULT 8

Q7TNB7_MOUSE

ID Q7TNB7_MOUSE PRELIMINARY; PRT; 720 AA.

AC Q7TNB7;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN Name=Rtn4;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

UN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6; TISSUE=Brain;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Bawastein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,

RA Bana S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Beak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Rahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J.W., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,

RA Scherich A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

UN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6; TISSUE=Brain;

RA Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC056373; AAH56373.1; -, mRNA.
 DR MGI; MGI:1915835; Rtn4.
 DR GO; GO:0042995; C:cell projection; IDA.
 DR GO; GO:0043025; C:cell soma; IDA.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0005155; F:protein binding; IPI.
 DR GO; GO:0001525; P:angiogenesis; IMP.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 KW Hypothetical protein.
 SQ SEQUENCE 720 AA; 77435 MW; 80AB78728F16EAB2 CRC64;

Query Match 86.0%; Score 119.5; DB 2; Length 720;
 Best Local Similarity 92.6%; Pred. No. 0.016;
 Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPDEDEDEDEDEDEDEDEDELEVL 27
 |||||:|||||
 Db 31 EPDEDEDEDEDEDEDEDEDELEVL 56

RESULT 9

ID QBGM9_MOUSE PRELIMINARY; PRT; 1162 AA.
 AC QBGM9;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Rtn4 (Reticulon 4).
 GN Name=Rtn4; ORFNames=RP23-17605.4-005;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/SvcJ7, and 129SvscJ7;
 RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
 RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
 RT "Genomic structure and functional characterisation of the promoters of
 human and mouse nogo/rtn4".
 RL J. Mol. Biol. 325:299-323(2003).
 RW [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/SvcJ7;
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/SvcJ7;
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]

RA Kay M.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY102284; AAM73506.1; -, mRNA.
 DR EMBL; AY102286; AAM73511.1; -, Genomic DNA.
 DR EMBL; AL929371; CA124273.1; -, Genomic DNA.
 DR Ensemble; ENSMUSG0000020458; Mus musculus.
 DR MGI; MGI:1915835; Rtn4.
 DR GO; GO:0042995; C:cell projection; IDA.
 DR GO; GO:0043025; C:cell soma; IDA.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0005155; F:protein binding; IPI.
 DR GO; GO:0001525; P:angiogenesis; IMP.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 1162 AA; 126612 MW; 855697FBEE11781F CRC64;

Query Match 86.0%; Score 119.5; DB 2; Length 1162;
 Best Local Similarity 92.6%; Pred. No. 0.024;
 Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPDEDEDEDEDEDEDEDEDELEVL 27
 |||||:|||||
 Db 31 EPDEDEDEDEDEDEDEDEDELEVL 56

RESULT 10

ID QBK3G_MOUSE PRELIMINARY; PRT; 1163 AA.
 AC QBK3G;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Nogo-A.
 GN Name=Rtn4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c;
 RA Jin W., Long M., Li R., Ju G.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY114152; NAM77068.1; -, mRNA.
 DR MGI; MGI:1915835; Rtn4
 DR GO; GO:0042995; C:cell projection; IDA.
 DR GO; GO:0043025; C:cell soma; IDA.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0005155; F:protein binding; IPI.
 DR GO; GO:0001525; P:angiogenesis; IMP.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 1163 AA; 126690 MW; 6B5F362799417EA4 CRC64;

Query Match 86.0%; Score 119.5; DB 2; Length 1163;
 Best Local Similarity 92.6%; Pred. No. 0.024;
 Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPDEDEDEDEDEDEDEDEDELEVL 27
 |||||:|||||
 Db 31 EPDEDEDEDEDEDEDEDEDELEVL 56

RESULT 11

ID QSDTK9_MOUSE PRELIMINARY; PRT; 1245 AA.
 AC QSDTK9;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE KIAA4153 protein (Fragment).
 GN Name=Rtn4; Synonym=KIAA4153;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE-Petal brain;
 RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Nagase T., Ohara O.,
 RA Koga H.;
 RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene.
 The Complete Nucleotide Sequences of Mouse KIAA-homologous cDNAs
 Identified by Screening of Terminal sequences of cDNA Clones Randomly

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RT Sampled from Size-Fractionated Libraries. ";
RL EMBL; AK220511; BAD90301.1; -; mRNA.
DR MGI; MGI:1915835; Rtn4.
DR GO; GO:0042995; C:cell projection; IDA.
DR GO; GO:0043025; C:cell soma; IDA.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0001525; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS00845; RETICULON; 1.
FT NON TER 1
SQ SEQUENCE 1245 AA; 135257 MW; 85460D746CE7F16C CRC64;

Query Match 86.0%; Score 119.5; DB 2; Length 1245;
Best Local Similarity 92.6%; Pred. No. 0.026;
Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPEDEDEDEDEDEDEDEDEDEDELEVL 27
Db 114 EPEDEDEDEDEDEDEDEDEDEDELEVL 139

RESULT 12
OS3R94 HUMAN
ID Q53R94 HUMAN PRELIMINARY; PRT; 185 AA.
AC Q53R94;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein Rtn4 (Fragment).
GN Name=Rtn4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kozlowicz A., Doebber A., Trani L.;
RA Kozlowicz A., Doebber A., Trani L.;
RA Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
RA EMBL; AC093165; AAY24029.1; -; Genomic DNA.
KW Hypothetical protein.
FT NON TER 185
SQ SEQUENCE 185 AA; 19300 MW; 568DF2FF3EBBF3E8 CRC64;

Query Match 80.2%; Score 111.5; DB 2; Length 185;
Best Local Similarity 85.2%; Pred. No. 0.022;
Matches 23; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPEDEDEDEDEDEDEDEDEDEDELEVL 27
Db 30 EPEDEDEDEDEDEDEDEDEDEDELEVL 55

RESULT 13
Q7L706 HUMAN
ID Q7L706_HUMAN PRELIMINARY; PRT; 373 AA.

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AC Q7L706;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DR RTN4 isoform B1.
GN Name=RTN4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Oestle T., Huber C., van der Putten H., Schwab M.E.;
RA "Genomic structure and functional characterisation of the promoters of
RT human and mouse nogo/rtn4.";
RT J. Mol. Biol. 325:299-323 (2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Van der Putten H.;
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY102277; AM64246.1; -; mRNA.
DR EMBL; AY102285; AM64241.1; -; Genomic DNA.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
SQ SEQUENCE 373 AA; 40317 MW; 8A19379EF91A59B4 CRC64;

Query Match 80.2%; Score 111.5; DB 2; Length 373;
Best Local Similarity 85.2%; Pred. No. 0.041;
Matches 23; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPEDEDEDEDEDEDEDEDEDEDELEVL 27
Db 30 EPEDEDEDEDEDEDEDEDEDEDELEVL 55

RESULT 14
Q96B16 HUMAN
ID Q96B16 HUMAN PRELIMINARY; PRT; 392 AA.
AC Q96B16;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Reticulon 4, isoform D (RTN4 isoform B2).
GN Name=RTN4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tissue=Kidney;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Casavant T.L., Scheetz T.E.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalish D.E.,
RA Scherf A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
human and mouse nogo/rtn4.";
RL J. Mol. Biol. 325:299-323 (2003).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016165; AAH16165.1; -; mRNA.
DR EMBL; AY102285; AAM64247.1; -; mRNA.
DR EMBL; AY102285; AAM64242.1; -; Genomic DNA.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS00845; RETICULON; 1.
SQ SEQUENCE 392 AA, 42274 MW, D7B2AA5E839B58AD CRC64;

Query Match 80.2%; Score 111.5; DB 2; Length 392;
Best Local Similarity 85.2%; Pred. NO. 0.043; 0; Indels 1; Gaps 1;
Matches 23; Conservative 3; Mismatches 0;

QY 1 EPDEDEDEDEDEDEDEDEDELELEVL 27
DB 30 EPDEDE-EEEEEDEDEDEDELELEVL 55

RESULT 15
RTN4 HUMAN
ID RTN4 HUMAN STANDARD; PRT; 1192 AA.
AC Q9NQC3; Q9A962; Q9BXG5; Q9H212; Q9H313; Q9U042; Q9Y293; Q9Y2V7;
AC Q9Y5U6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foccon)
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific
protein C homolog) (RTN-x) (Reticulon 5).
DE Name=RTN4; Synonyms=ASY, KIAA0886, NOGO; ORFNames=My043, SP1507;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;
RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,
Michaelovich D., Simmons D.L., Walsh F.S.;
RT "Inhibitor of neurite outgrowth in humans.";
RL Nature 403:383-384 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=21010696; PubMed=11126360; DOI=10.1038/sj.onc.1203948;
RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
endoplasmic reticulum and reduces their anti-apoptotic activity.";
RL Oncogene 19:5736-5746 (2000).
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20237542; PubMed=10773680;
RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;
RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome
2p14--2p13 by radiation hybrid mapping.";

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RL Cytogetet. Cell Genet. 88:101-102 (2000).
RN [4]
RP NUCLEOTIDE SEQUENCE (ISOFORM 4).
RA Jin W.-L., Ju G.;
RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 2 AND 3).
RC TISSUE=Placenta, and Skeletal muscle;
RA Ito T., Schwartz S.M.;
RT "Cloning of a member of the reticulon gene family in human.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC TISSUE=Fibroblast;
RA Yutsudo M.;
RT "Isolation of a cell death-inducing gene.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE (ISOFORM 3).
RC TISSUE=Pituitary;
RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
Luo B., Hu R., Chen J.;
RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [8]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RX PubMed=15498874; DOI=10.1073/pnas.0404089101;
RA Wan D., Gong Y., Qin W., Zhang P., Li J., Wei L., Zhou X., Li H.,
Qiu X., Zhong F., He L., Yu J., Yao G., Jiang H., Qian L., Yu Y.,
Shu H., Chen X., Xu H., Guo M., Pan Z., Chen Y., Ge C., Yang S.,
Gu J.;
RT "Large-scale cDNA transfection screening for genes related to cancer
development and progression.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:15724-15729 (2004).
RN [9]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485;
RA Magase I., Ishikawa K.-I., Suyama M., Kikuno R., Hirosewa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
RL DNA Res. 5:355-364 (1998).
RN [10]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 2 AND 3).
RC TISSUE=Brain, Eye, Ovary, Pancreas, Placenta, and Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Haefl F.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heif F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boesk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
Schurch A., Schein J.S., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [11]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC TISSUE=Umbilical cord blood;
RX MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;

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RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.-
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
RT "Cloning and functional analysis of cDNAs with open reading frames for
RT 300 previously undefined genes expressed in CD34+ hematopoietic
RT stem/progenitor cells.";
RL Genome Res. 10:1546-1560(2000).
RN
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 482-1192 (ISOFORMS 1/4).
RC TISSUE=Petal brain;
RC Mac Y.M., Xie Y., Zheng Z.H.;
RA Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RL
RN NUCLEOTIDE SEQUENCE OF 186-1192 (ISOFORM 1).
RC TISSUE=Testis;
RC Sha J.H., Zhou Z.M., Li J.M.;
RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RL
RN
RN TOPOLOGY.
RC TISSUE=Brain;
RC MEDLINE=21069055; PubMed=10667797; DOI=10.1038/35000226;
RX Fournier A.E., Grandpre T., Strittmatter S.M.;
RA "Identification of a receptor mediating Nogo-66 inhibition of axonal
RT regeneration.";
RT Reticulon Protein.";
RL Nature 409:341-346(2001).
RN
RN FUNCTION.
RC TISSUE=Brain;
RC MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;
RX Fournier A.E., Grandpre T., Strittmatter S.M.;
RA "Identification of a receptor mediating Nogo-66 inhibition of axonal
RT regeneration.";
RT Reticulon Protein.";
RL Nature 409:341-346(2001).
RN
RN REVIEW.
RC MEDLINE=21888956; PubMed=11891768; DOI=10.1002/jnr.10134;
RX Ng C.E.L., Tang B.L.;
RA "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
RT regeneration.";
RT J. Neurosci. Res. 67:559-565(2002).
RL
CC -I- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC block the regeneration of the nervous central system in adults.
CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.
CC This is likely consecutive to their change in subcellular
CC location, from the mitochondria to the endoplasmic reticulum,
CC after binding and sequestration.
CC -I- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum. Anchored to the membrane of the endoplasmic reticulum
CC through 2 putative transmembrane domains.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-XL;
CC IsoId=Q9NQC3-1; Sequence=Displayed;
CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-XS, Foccen-M;
CC IsoId=Q9NQC3-2; Sequence=VSP_005655;
CC Name=3; Synonyms=RTN 4C, Nogo-C, Foccen-S;
CC IsoId=Q9NQC3-3; Sequence=VSP_005652, VSP_005653;
CC Name=4;
CC IsoId=Q9NQC3-4; Sequence=VSP_005654;
CC -I- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain
CC and testis and weakly in heart and skeletal muscle. Isoform 2 is
CC widely expressed excepted for the liver. Isoform 3 is expressed in
CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-
CC specific.
CC -I- SIMILARITY: Contains 1 reticulon domain.
CC -I- CAUTION: Ref.11 sequence differs from that shown due to
CC framehifts in positions 1149 and 1156.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not

removed.
CC EMBL; AJ251383; CAB99248.1; -; mRNA.
DR EMBL; AJ251384; CAB99249.1; -; mRNA.
DR EMBL; AJ251385; CAB99250.1; -; mRNA.
DR EMBL; AB040462; BAB18927.1; -; mRNA.
DR EMBL; AB040463; BAB18928.1; -; mRNA.
DR EMBL; AF148537; AAG12176.1; -; mRNA.
DR EMBL; AF148538; AAG12177.1; -; mRNA.
DR EMBL; AF087901; AAG12205.1; -; mRNA.
DR EMBL; AF320999; AAG40878.1; -; mRNA.
DR EMBL; AF132047; AAD31021.1; -; mRNA.
DR EMBL; AF132048; AAD31022.1; -; mRNA.
DR EMBL; AB015639; BAA83712.1; -; mRNA.
DR EMBL; AF077050; AAD27783.1; -; mRNA.
DR EMBL; AF177332; AAG17976.1; -; mRNA.
DR EMBL; AB020693; BAA74909.2; ALT INIT; mRNA.
DR EMBL; BC001035; BAA1035.1; -; mRNA.
Query Match 80.2%; Score 111.5; DB 1; Length 1192;
Best Local Similarity 85.2%; Pred. No. 0.12;
Matches 23; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
QY 1 EPDEDEDEDEDEDEDEDEDEDELEVL 27
DB 30 EPDEDEDEDEDEDEDEDEDEDELEVL 55
Search completed: February 17, 2006, 03:55:48
Job time : 125.333 secs

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OM protein - protein search, using sw model

Run on: February 17, 2006, 03:56:08 ; Search time 28.6667 Seconds
(without alignments)
77.869 Million cell updates/sec

Title: US-09-830-972A-2_COPY_31_57
Perfect score: 139
Sequence: 1 EPDEDEDEDEDEDEDEDELEVL 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/aaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/aaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/aaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/aaa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/aaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/aaa/backfileal.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
Result No.	Score	Query Match %	DB ID		
1	111.5	80.2	US-09-513-999C-6304	Sequence 6304, Ap	
2	97	69.8	US-09-538-092-1018	Sequence 1018, Ap	
3	97	69.8	US-09-214-881A-2	Sequence 2, Appli	
4	97	69.8	US-09-949-016-10728	Sequence 10728, A	
5	97	69.8	US-08-339-152A-32	Sequence 32, Appl	
6	93	66.3	US-09-949-016-8301	Sequence 8301, Ap	
7	92	66.2	US-08-248-796A-15347	Sequence 15347, A	
8	92	66.2	US-08-574-959A-9	Sequence 9, Appli	
9	92	66.2	US-03-357-014-9	Sequence 9, Appli	
10	92	66.2	US-08-574-959A-7	Sequence 7, Appli	
11	92	66.2	US-09-357-014-7	Sequence 7, Appli	
12	91	65.5	US-09-214-881A-8	Sequence 8, Appli	
13	91	65.5	US-09-214-881A-6	Sequence 6, Appli	
14	90.5	65.1	US-09-214-881A-6	Sequence 6, Appli	
15	90	64.7	US-09-248-796A-22092	Sequence 22092, A	
16	90	64.7	US-08-114-555A-8	Sequence 8, Appli	
17	90	64.7	US-09-538-092-1018	Sequence 8, Appli	
18	90	64.7	US-09-424-783-4	Sequence 14, Appli	
19	88	63.3	US-08-741-134-2	Sequence 2, Appli	
20	88	63.3	US-10-104-047-2973	Sequence 2973, Ap	
21	87	62.6	US-09-214-881A-9	Sequence 9, Appli	
22	87	62.6	US-09-538-092-883	Sequence 883, App	
23	87	62.6	US-09-214-881A-1	Sequence 1, Appli	
24	87	62.6	US-08-990-114-3	Sequence 3, Appli	
25	87	62.6	US-09-241-333-3	Sequence 3, Appli	
26	86	61.9	US-10-104-047-2651	Sequence 2651, Ap	
27	86	61.9	US-09-538-092-957	Sequence 957, App	

ALIGNMENTS				Description	
Result No.	Score	Query Match %	DB ID		
1	111.5	80.2	US-09-513-999C-6304	Sequence 6304, Ap	
2	97	69.8	US-09-538-092-1018	Sequence 1018, Ap	
3	97	69.8	US-09-214-881A-2	Sequence 2, Appli	
4	97	69.8	US-09-949-016-10728	Sequence 10728, A	
5	97	69.8	US-08-339-152A-32	Sequence 32, Appl	
6	93	66.3	US-09-949-016-8301	Sequence 8301, Ap	
7	92	66.2	US-08-248-796A-15347	Sequence 15347, A	
8	92	66.2	US-08-574-959A-9	Sequence 9, Appli	
9	92	66.2	US-03-357-014-9	Sequence 9, Appli	
10	92	66.2	US-08-574-959A-7	Sequence 7, Appli	
11	92	66.2	US-09-357-014-7	Sequence 7, Appli	
12	91	65.5	US-09-214-881A-8	Sequence 8, Appli	
13	91	65.5	US-09-214-881A-6	Sequence 6, Appli	
14	90.5	65.1	US-09-214-881A-6	Sequence 6, Appli	
15	90	64.7	US-09-248-796A-22092	Sequence 22092, A	
16	90	64.7	US-08-114-555A-8	Sequence 8, Appli	
17	90	64.7	US-09-538-092-1018	Sequence 8, Appli	
18	90	64.7	US-09-424-783-4	Sequence 14, Appli	
19	88	63.3	US-08-741-134-2	Sequence 2, Appli	
20	88	63.3	US-10-104-047-2973	Sequence 2973, Ap	
21	87	62.6	US-09-214-881A-9	Sequence 9, Appli	
22	87	62.6	US-09-538-092-883	Sequence 883, App	
23	87	62.6	US-09-214-881A-1	Sequence 1, Appli	
24	87	62.6	US-08-990-114-3	Sequence 3, Appli	
25	87	62.6	US-09-241-333-3	Sequence 3, Appli	
26	86	61.9	US-10-104-047-2651	Sequence 2651, Ap	
27	86	61.9	US-09-538-092-957	Sequence 957, App	

RESULT 1
US-09-513-999C-6304
Sequence 6304, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59 US2 REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 6304
LENGTH: 68
TYPE: PRT
ORGANISM: Homo sapiens
US-09-513-999C-6304

Query Match 80.2%; Score 111.5; DB 2; Length 68;
Best Local Similarity 85.2%; Pred. No. 2.7e-05;
Matches 23; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 1 EPDEDEDEDEDEDEDEDELEVL 27
Db 30 EPDEDE-EEDEDEDEDEDELEVL 55

RESULT 2
US-09-538-092-1018
Sequence 1018, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Glot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurPatSeqFormatter Version 0.9
SEQ ID NO 1018

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; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P26583
US-09-538-092-1018

Query Match          69.8%; Score 97; DB 2; Length 208;
Best Local Similarity 73.9%; Pred. No. 0.0024;
Matches 17; Conservative

QY 1 EPEDEDEDEDEDEDEDELE 23
Db 185 EPEDEDEDEDEDEDEDEDEDEDE 207

RESULT 3
US-09-214-881A-2
; Sequence 2, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuo
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hicoshi
; APPLICANT: Okakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-881A-2

Query Match          69.8%; Score 97; DB 2; Length 208;
Best Local Similarity 73.9%; Pred. No. 0.0024;
Matches 17; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDELE 23
Db 185 EPEDEDEDEDEDEDEDEDEDEDE 207

RESULT 4
US-09-949-016-10728
; Sequence 10728, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 10728

; LENGTH: 320
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10728

Query Match          69.8%; Score 97; DB 2; Length 320;
Best Local Similarity 73.9%; Pred. No. 0.0036;
Matches 17; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDELE 23
Db 297 EPEDEDEDEDEDEDEDEDEDEDE 319

RESULT 5
US-08-339-152A-32
; Sequence 32, Application US/08339152A
; Patent No. 5643726
; GENERAL INFORMATION:
; APPLICANT: Tanzil, Rudolph E.
; APPLICANT: Kovacs, Dora M.
; TITLE OF INVENTION: Methods For Modulating Transcription
; FROM The Amyloid -Protein Precursor (APP) Promoter
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,152A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 0609.4120000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-339-152A-32

Query Match          69.8%; Score 97; DB 1; Length 532;
Best Local Similarity 80.0%; Pred. No. 0.0058;
Matches 20; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 3 EDEDEDEDEDEDEDEDEDEDEDELE 25
Db 172 EDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 196

RESULT 6
US-09-949-016-8301
; Sequence 8301, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
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us-09-830-972a-2_copy_31_57.ra1

Tue Feb 21 15:13:29 2006

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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8301
; LENGTH: 2079
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8301

Query Match 66.9%; Score 93; DB 2; Length 2079;
Best Local Similarity 72.0%; Pred. No. 0.053;
Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDELE 25
Db 1077 EEEEEEEEEEEEEDEEE 1101

RESULT 7
US-09-248-796A-15347
; Sequence 15347, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15347
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15347

Query Match 66.2%; Score 92; DB 2; Length 448;
Best Local Similarity 77.3%; Pred. No. 0.016;
Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 EDEDEDEDEDEDEDELE 24
Db 410 DEEEDEDEDEDEDEEE 431

RESULT 8
US-08-574-959A-9
; Sequence 9, Application US/08574959A
; Patent No. 5962224
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Inail Joong, Ratna K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/574,959A
; APPLICATION NUMBER: US/08/574,959A
; FILING DATE: 19-DEC-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 905 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-574-959A-9

Query Match 66.2%; Score 92; DB 1; Length 905;
Best Local Similarity 68.0%; Pred. No. 0.031;
Matches 17; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDELE 25
Db 665 EEEEEEEEEEEEEDEEE 689

RESULT 9
US-09-357-014-9
; Sequence 9, Application US/09357014
; Patent No. 6291645
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Inail Joong, Ratna K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/357,014
; FILING DATE: 19-Jul-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/574,959
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 905 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-357-014-9

Query Match      66.2%; Score 92; DB 2; Length 905;
Best Local Similarity 68.0%; Pred. No. 0.031;
Matches 17; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      1 EPDEDEDEDEDEDEDEDEDELE 25
DB      665 EEEDEDEDEDEDEDEDEDEEE 689

RESULT 10
US-08-574-959A-7
; Sequence 7, Application US/08574959A
; Patent No. 5962224
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Insil Jeoung, Ratna K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: P62 POLYPEPTIDES, RELATED POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/574,959A
; FILING DATE: 19-DEC-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-574-959A-7

Query Match      66.2%; Score 92; DB 1; Length 1135;
Best Local Similarity 68.0%; Pred. No. 0.038;
Matches 17; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      1 EPDEDEDEDEDEDEDEDEDELE 25
DB      895 EEEDEDEDEDEDEDEDEDEEE 919

RESULT 11
US-09-357-014-7
; Sequence 7, Application US/09357014
; Patent No. 6291645
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Insil Jeoung, Ratna K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: P62 POLYPEPTIDES, RELATED POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/574,959A
; FILING DATE: 19-DEC-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-574-959A-7

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 17, 2006, 03:58:38 ; Search time 8.66667 Seconds
(without alignments)
44.284 Million cell updates/sec

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Perfect score: 139
Sequence: 1 EPEDEDEDEDEDEDEDELEVL 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA New.*
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2: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pap.*
3: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pap.*
4: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB.pap.*
5: /cgn2_6/prodata/1/pubppa/US09_NEW_PUB.pap.*
6: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB.pap.*
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8: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	100.0	1163	7	US-11-044-899-2
2	139	100.0	1163	7	US-11-044-899-2
3	111.5	80.2	414	6	US-10-821-234-1170
4	111.5	80.2	1178	7	US-11-044-899-29
5	88	63.3	683	7	US-11-072-512-2973
6	88	63.3	773	7	US-11-169-041-213
7	87	62.6	215	6	US-10-821-234-143
8	86	61.9	482	6	US-10-821-234-143
9	86	61.9	687	7	US-11-072-512-2631
10	84	60.4	144	6	US-10-821-234-1254
11	83	59.7	251	6	US-10-528-031-8
12	83	59.7	345	7	US-11-024-959-415
13	82	59.0	1299	7	US-11-054-281-107
14	81	58.3	417	6	US-10-821-234-1536
15	81	58.3	740	7	US-11-124-367A-293
16	81	58.3	760	7	US-11-124-367A-292
17	81	58.3	823	7	US-11-166-892-4
18	79	55.8	268	7	US-11-072-512-3158
19	79	55.8	879	7	US-11-169-041-192
20	78	56.1	3375	7	US-11-044-111-23
21	77.5	55.8	587	6	US-10-453-372-964
22	77.5	55.8	591	6	US-10-453-372-952
23	77.5	55.8	591	6	US-10-453-372-956
24	77.5	55.8	596	6	US-10-453-372-954
25	77.5	55.8	642	6	US-10-453-372-962

26	77.5	55.8	646	6	US-10-453-372-958
27	77.5	55.8	646	6	US-10-453-372-960
28	77.5	55.8	687	7	US-11-156-163-4
29	77.5	55.8	688	6	US-10-453-372-950
30	77.5	55.8	688	6	US-10-453-372-968
31	77.5	55.8	688	6	US-10-453-372-970
32	77	55.4	427	9	US-10-718-807-122
33	77	55.4	699	7	US-11-138-682-4
34	77	55.4	699	7	US-11-138-682-4
35	77	55.4	4374	7	US-11-128-572-2
36	76.5	55.0	645	6	US-10-821-234-1409
37	76	54.7	432	7	US-11-055-822-1096
38	75	54.0	298	6	US-10-821-234-1167
39	75	54.0	476	7	US-11-124-368A-261
40	75	54.0	619	7	US-11-124-368A-260
41	75	54.0	655	7	US-11-124-368A-262
42	75	54.0	671	7	US-11-124-368A-259
43	75	54.0	763	6	US-10-821-234-1619
44	75	54.0	1017	7	US-11-054-281-108
45	75	54.0	1061	7	US-11-121-438-4

ALIGNMENTS

RESULT 1
US-11-044-899-2
; Sequence 2, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED THEREON
; FILE OF INVENTION: 0200-017-999
; FILE REFERENCE: 0200-017-999
; CURRENT APPLICATION NUMBER: US/11/044,899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830,972
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus sp.
US-11-044-899-2

Query Match 100.0%; Score 139; DB 7; Length 1163;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDELEVL 27
DB 31 EPEDEDEDEDEDEDELEVL 57

RESULT 2
US-11-044-899-30
; Sequence 30, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED THEREON
; FILE OF INVENTION: 10200-017-999
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044,899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830,972


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US-11-169-041-213
; Sequence 213, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 213
; LENGTH: 773
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-213
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Best Local Similarity 64.0%; Pred. No. 0.0066;
Matches 16; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
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DB 485 EEEDEDEDEDEDEDEDETESE 509
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RESULT 7
US-10-821-234-1443
; Sequence 1443, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pt-Seq_genes Version 1.0
; SEQ ID NO 1443
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1443
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Query Match 62.6%; Score 87; DB 6; Length 215;
Best Local Similarity 65.2%; Pred. No. 0.0023;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
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DB 190 DEEDEDEDEDEDEDEEDD 212
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US-10-821-234-1413
; Sequence 1413, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
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; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pt-Seq_genes Version 1.0
; SEQ ID NO 1413
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1413
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Best Local Similarity 56.0%; Pred. No. 0.0068;
Matches 14; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
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DB 147 EEEDEDEDEDEDEDEDEIE 171
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RESULT 9
US-11-072-512-2651
; Sequence 2651, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: MAKANATSU, AI
; APPLICANT: SATO, HIROVUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YUKI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2651
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2651
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Query Match 61.9%; Score 86; DB 7; Length 687;
Best Local Similarity 56.0%; Pred. No. 0.0097;
Matches 14; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
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QY 1 EPDEDEDEDEDEDEDEDELEE 25
DB 124 EEEDEDEDEDEDEDEDEIE 148
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RESULT 10
US-10-821-234-1254
; Sequence 1254, Application US/10821234
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; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1254
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1254

Query Match      60.4%; Score 84; DB 6; Length 144;
Best Local Similarity 56.0%; Pred. No. 0.0033;
Matches 14; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

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Db      97 DDEDEDDDEDEDEDEDEDEE 121

RESULT 11
US-10-528-031-8
; Publication No. US20050262577A1
; GENERAL INFORMATION:
; APPLICANT: ORIDIS BIOMED FORSCHUNGS- und ENTWICKLUNGS GmbH
; APPLICANT: Guelly, Christian
; APPLICANT: Buck, Charles R.
; APPLICANT: Zalcoukaki, Kuri
; TITLE OF INVENTION: Polypeptides and nucleic acids encoding these and their use for
; FILE OF INVENTION: Prevention, diagnosis or treatment of liver disorders and epit
; FILE REFERENCE: Oridis Biomed
; CURRENT APPLICATION NUMBER: US/10/528,031
; CURRENT FILING DATE: 2005-03-16
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-528-031-8

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Best Local Similarity 59.6%; Pred. No. 0.0074; 3; Indels 0; Gaps 0;
Matches 16; Conservative 4; Mismatches 4;

Qy      3 EDEDEDEDEDEDEDEDELE 25
Db      167 EEEDEGEDEDEDDDDGDEEE 189

RESULT 12
US-11-024-959-415
; Sequence 415, Application US/11024959
; Publication No. US20060010516A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGINS, COLLEEN M.
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: KODRZYCKI, BOB

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; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_SEQ_genes Version 1.0
; SEQ ID NO 1536
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-1536

Query Match      58.3%; Score 81; DB 6; Length 417;
Best Local Similarity 56.0%; Pred. NO. 0.02;
Matches 14; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Qy      1 EPDEDEDEDEDEDEDEDEDELELE 25
Db      381 EADKEDDEDEDEDEDEDEDEDE 405

RESULT 15
US-11-124-367A-293
; Sequence 293, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124.367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 293
; LENGTH: 740
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-124-367A-293

Query Match      58.3%; Score 81; DB 7; Length 740;
Best Local Similarity 51.6%; Pred. NO. 0.036;
Matches 16; Conservative 7; Mismatches 2; Indels 6; Gaps 1;

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Db      441 ERSDEDEDEDEDEDEDEDEDEDEDEDELE 471

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